

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 07:50:48 ; Search time 93.7895 Seconds  
(without alignment)  
28.108 Million cell updates/sec

Title: US-09-868-131C-45

Perfect score: 6

Sequence: 1 FXXXXX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq 21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003ba.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	2	1 AAP10185	Aap10185 Sequence
2	6	100.0	2	1 AAB27796	Aab27796 Human sec
3	6	100.0	2	4 AAB91687	Aab91687 Opioid pe
4	6	100.0	2	4 AAB91888	Aab91888 Apoptosis
5	6	100.0	2	4 AAB91688	Aab91688 Opioid pe
6	6	100.0	2	4 AAB91578	Aab91578 Opioid pe
7	6	100.0	2	4 AAB91037	Aab91037 Thyrotrop
8	6	100.0	2	4 AAB91857	Aab91857 Antimicro
9	6	100.0	2	5 ABG64373	Abg64373 Human alb
10	6	100.0	2	5 ABG63747	Abg63747 Human alb
11	6	100.0	2	7 ADW36932	Adw36932 HLA bindi
12	6	100.0	2	7 ADW36737	Adw36737 HLA bindi
13	6	100.0	2	7 ADW36731	Adw36731 HLA bindi
14	6	100.0	2	7 ADW36724	Adw36724 HLA bindi
15	6	100.0	2	7 ADW36724	Adw36724 HLA bindi
16	6	100.0	2	8 ADL77012	Adl77012 Albumin f
17	6	100.0	2	8 ADL77640	Adl77640 Albumin f
18	6	100.0	2	8 ADU07108	Adu07108 Fungal gr
19	6	100.0	3	1 AAP20375	Aap20375 Analgesic
20	6	100.0	3	1 AAP60186	Aap60186 Renin-inh
21	6	100.0	3	1 AAP82709	Aap82709 Renin inh
22	6	100.0	3	2 AAR29096	Aar29096 Cathepsin
23	6	100.0	3	2 AAR38411	Aar38411 Cathepsin
24	6	100.0	3	2 AAR39998	Aar39998 Scintigra

25	6	100.0	3	2 AAR59333	Aar59333 HIV prote
26	6	100.0	3	2 AAR47530	Aar47530 GHRP-6 an
27	6	100.0	3	2 AAR47853	Aar47853 Galpain i
28	6	100.0	3	2 AAR53239	Aar53239 Heparin d
29	6	100.0	3	2 AAR63264	Aar63264 Thrombin
30	6	100.0	3	2 AAR63263	Aar63263 Thrombin
31	6	100.0	3	2 AAR63261	Aar63261 Thrombin
32	6	100.0	3	2 AAR63260	Aar63260 Thrombin
33	6	100.0	3	2 AAR63262	Aar63262 Thrombin
34	6	100.0	3	2 AAR47430	Aar47430 ACE inhib
35	6	100.0	3	2 AAR61093	Aar61093 ACE-inhib
36	6	100.0	3	2 AAR58581	Aar58581 Angiotens
37	6	100.0	3	2 AAR58575	Aar58575 Angiotens
38	6	100.0	3	2 AAR58576	Aar58576 Angiotens
39	6	100.0	3	2 AAR58578	Aar58578 Angiotens
40	6	100.0	3	2 AAR58570	Aar58570 Angiotens
41	6	100.0	3	2 AAR58579	Aar58579 Angiotens
42	6	100.0	3	2 AAR58572	Aar58572 Angiotens
43	6	100.0	3	2 AAR58577	Aar58577 Angiotens
44	6	100.0	3	2 AAR58574	Aar58574 Angiotens
45	6	100.0	3	2 AAR58580	Aar58580 Angiotens
46	6	100.0	3	2 AAR63378	Aar63378 Delta opi
47	6	100.0	3	2 AAR69779	Aar69779 Thrombos
48	6	100.0	3	2 AAR85069	Aar85069 Calcium i
49	6	100.0	3	2 AAR64556	Aar64556 RF-1 pept
50	6	100.0	3	2 AAR64365	Aar64365 DP-178 ho
51	6	100.0	3	2 AAR98166	Aar98166 Peptide f
52	6	100.0	3	2 AAR88897	Aar88897 Small syn
53	6	100.0	3	2 AAR88899	Aar88899 Small syn
54	6	100.0	3	2 AAR88900	Aar88900 Small syn
55	6	100.0	3	2 AAR88898	Aar88898 Small syn
56	6	100.0	3	2 AAR02320	Aar02320 Beta-amyl
57	6	100.0	3	2 AAR02319	Aar02319 Beta-amyl
58	6	100.0	3	2 AAR00269	Aar00269 Cytokine
59	6	100.0	3	2 AAR18871	Aar18871 Peptide f
60	6	100.0	3	2 AAR33241	Aar33241 Analgesic
61	6	100.0	3	2 AAR31134	Aar31134 Atheroscl
62	6	100.0	3	2 AAR56233	Aar56233 Anti-infl
63	6	100.0	3	2 AAR56203	Aar56203 Anti-infl
64	6	100.0	3	2 AAR56218	Aar56218 Anti-infl
65	6	100.0	3	2 AAR56179	Aar56179 Anti-infl
66	6	100.0	3	2 AAR64741	Aar64741 Angiotens
67	6	100.0	3	2 AAR52446	Aar52446 Loop regi
68	6	100.0	3	2 AAR61936	Aar61936 PPI bindi
69	6	100.0	3	2 AAR76946	Aar76946 Fusion im
70	6	100.0	3	2 AAR71123	Aar71123 Peptide A
71	6	100.0	3	2 AAR40485	Aar40485 SH2 bindi
72	6	100.0	3	2 AAR31654	Aar31654 Human cyt
73	6	100.0	3	2 AAY04709	Aay04709 Mouse RPT
74	6	100.0	3	2 AAY30619	Aay30619 Amino aci
75	6	100.0	3	2 AAR84197	Aar84197 Peptide c
76	6	100.0	3	2 AAY30579	Aay30579 Amino aci
77	6	100.0	3	2 AAY39891	Aay39891 Asparagin
78	6	100.0	3	2 AAB09713	Aab09713 Insulin l
79	6	100.0	3	3 AAB22907	Aab22907 Cathepsin
80	6	100.0	3	3 AAB23987	Aab23987 Linker pe
81	6	100.0	3	3 AAB23991	Aab23991 Linker pe
82	6	100.0	3	3 AAB23951	Aab23951 Amino aci
83	6	100.0	3	3 AAY68621	Aay68621 Light cha
84	6	100.0	3	3 AAY32259	Aay32259 Morphine
85	6	100.0	3	3 AAY49399	Aay49399 Beta-caso
86	6	100.0	3	3 AAY49409	Aay49409 Novel aut
87	6	100.0	3	3 AAY49387	Aay49387 Dermorphi
88	6	100.0	3	3 AAY79609	Aay79609 Cathepsin
89	6	100.0	3	3 AAY97169	Aay97169 Human Abe
90	6	100.0	3	3 AAB37934	Aab37934 Trypsin m
91	6	100.0	3	3 AAB37932	Aab37932 Trypsin m
92	6	100.0	3	3 AAB37930	Aab37930 Trypsin m
93	6	100.0	3	3 AAB37941	Aab37941 Trypsin m
94	6	100.0	3	3 AAB37940	Aab37940 Trypsin m
95	6	100.0	3	3 AAB63094	Aab63094 Human sec
96	6	100.0	3	4 AAM97080	Aam97080 Human pep
97	6	100.0	3	4 AAM98085	Aam98085 Human pep

98 6 100.0 3 4 AAB72278 Aab72278 Colostrin  
 99 6 100.0 3 4 AAB91589 Aab91589 Opioid pe  
 100 6 100.0 3 4 AAB91580 Aab91580 Opioid pe

## ALIGNMENTS

RESULT 1  
 AAB10185  
 ID AAB10185 standard; protein; 2 AA.  
 XX  
 AC AAB10185;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 16-AUG-2002 (revised)  
 DT 14-AUG-1992 (first entry)  
 XX  
 DE Sequence of synthetic polypeptide for the prodn. of aspartame.  
 XX  
 KW Aspartyl-phenylalanine methyl ester; artificial sweetener; aspartame.

XX Synthetic.  
 XX EP36258-A.  
 XX  
 PD 23-SEP-1981.  
 XX  
 PF 14-MAR-1980; 80US-00130462.  
 XX  
 PR 14-MAR-1980; 80US-00130462.  
 XX  
 PA (CETU ) CETUS CORP.  
 XX  
 PI Rose JE, White TJ, Bahl CP;  
 XX  
 DR WPI; 1981-72133D/40.  
 DR N-PSDB; AAN10059.

XX Aspartame prodn. from synthetic polypeptide - produced by cloned microorganism.

PS Disclosure; Page 5; 18pp; English.

XX The inventors claim a method for the prodn. of aspartame by first synthesising double-stranded DNA in which a coding strand has alternating codons for Asp and the Phe in sufficient number to produce a polypeptide which is stable in predetermined host microorganisms. The DNA strand is then inserted into a cloning vehicle so that the resulting chimera directs the synthesis of the Asp-Phe protein. This protein is then cleaved with CNBr or trypsin to release the peptide which, after benzylation, can be fragmented by digestion with chymotrypsin. (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 1; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 2 F 2

RESULT 2  
 AAB27796  
 ID AAB27796 standard; protein; 2 AA.  
 XX  
 AC AAB27796;  
 XX  
 DT 29-JAN-2001 (first entry)

XX Human secreted protein #3.  
 DE  
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200055199-A1.

XX 21-SEP-2000.

XX 09-MAR-2000; 2000WO-US006014.

XX 12-MAR-1999; 99US-0124095P.

XX 11-JUN-1999; 99US-0138598P.

XX 03-DEC-1999; 99US-0168663P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM, Komatsoulis G;

XX WPI; 2000-572359/53.

XX N-PSDB; AAC59217.

XX Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX Claim 11; Page 371-372; 433pp; English.

XX Sequences AAB27794-B27840 represent the amino acid sequences of 47 human secreted proteins encoded by the genes AAC59215-C59261. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections

XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 3; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 1 F 1

RESULT 3  
 AAB91687  
 ID AAB91687 standard; peptide; 2 AA.  
 XX  
 AC AAB91687;  
 XX  
 DT 22-JUN-2001 (first entry)

XX Opioid peptide SEQ ID NO:863.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimide; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
PI WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.  
XX Disclosure; Page 477; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention

XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 2 F 2

RESULT 4

AAB91888  
ID AAB91888 standard; peptide; 2 AA.

XX AAB91888;

XX 22-JUN-2001 (first entry)

XX Apoptosis related peptide SEQ ID NO:1064.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.  
XX Disclosure; Page 543; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention

XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 2 F 2

RESULT 5

AAB91888  
ID AAB91888 standard; peptide; 2 AA.

XX AAB91888;

XX 22-JUN-2001 (first entry)

XX Opioid peptide SEQ ID NO:864.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.





PS Disclosure; Page 258; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention

XX Sequence 2 AA;

SQ Sequence 2 AA;

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 8  
AAB91857  
ID AAB91857 standard; peptide; 2 AA.

XX AAB91857;  
AC  
XX  
DT 22-JUN-2001 (first entry)

XX Antimicrobial peptide SEQ ID NO:1033.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.  
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 533; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention

XX Sequence 2 AA;

SQ Sequence 2 AA;

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 9  
ABG64373  
ID ABG64373 standard; protein; 2 AA.

XX AC ABG64373;

XX 27-AUG-2002 (first entry)

XX Human albumin fusion protein #1048.

XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
KW human serum albumin; HSA; cancer; reproductive disorder;  
KW digestive disorder; immune disorder; endocrine disorder;  
KW haematopoietic disorder; neural disorder; connective disorder;  
KW cytostatic; antiinfectility; antiinflammatory; antitumor;  
KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;  
KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
KW osteopathic; antiarthritic.

XX Homo sapiens.

OS Synthetic.

XX WO200177137-A1.

XX 18-OCT-2001.

XX 12-APR-2001; 2001WO-US011989.

XX 12-APR-2000; 2000US-0229358P.

PR 25-APR-2000; 2000US-0199384P.

PR 21-DEC-2000; 2000US-0256931P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Haseeltine WA;

XX WPI; 2002-010886/01.

XX New fusion protein for treating disease e.g. diabetes comprises an

XX albumin fused to a therapeutic protein.

XX Claim 1; Page 1158; 2102pp; English.

XX The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo

CC activity. The protein is useful for treating and diagnosing disorders  
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
 CC disease, ulcerative colitis), immune disorders (e.g. acquired  
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,  
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
 XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 5; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 2 F 2

#### RESULT 10

ID ABG63747 standard; protein; 2 AA.

XX AC ABG63747;

XX DT 27-AUG-2002 (first entry)

XX DE Human albumin fusion protein #422.

XX KW Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytostatic; antiinfertility; antiinflammatory; antiulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200177137-A1.

XX PD 18-OCT-2001.

XX PF 12-APR-2001; 2001WO-US011988.

XX PR 12-APR-2000; 2000US-0229358P.

XX PR 25-APR-2000; 2000US-0199384P.

XX PR 21-DEC-2000; 2000US-0256931P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Haseltine WA;

XX DR WPI; 2002-010886/01.

XX PT New fusion protein for treating disease e.g. diabetes comprises an

XX PT albumin fused to a therapeutic protein.

XX PS Claim 1; Page 820; 2102pp; English.

XX CC The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or disorder  
 CC that may be modulated by therapeutic protein X. The albumin extends the  
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo  
 CC activity. The protein is useful for treating and diagnosing disorders  
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
 CC disease, ulcerative colitis), immune disorders (e.g. acquired  
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,

CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
 XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 5; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 Db 1 F 1

#### RESULT 11

ADW36932

ID ADW36932 standard; peptide; 2 AA.

XX AC ADW36932;

XX DT 10-MAR-2005 (first entry)

XX DE HLA binding epitope #7682.

XX KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
 KW viral disease; cancer.

XX OS Unidentified.

XX PN WO2003040165-A2.

XX PD 15-MAY-2003.

XX PF 18-OCT-2001; 2001WO-US051650.

XX PR 19-OCT-2000; 2000US-0242350P.

XX PR 20-APR-2001; 2001US-0285624P.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S;

XX DR WPI; 2003-441519/41.

XX PT New composition comprising at least one peptide having allele-specific  
 PT binding motifs for HLA, useful for preventing, treating or diagnosing  
 PT viral diseases and cancer.

XX PS Claim 1; Page 52-379; 382pp; English.

XX CC The invention relates to a composition comprising at least one peptide  
 CC having an isolated, prepared epitope selected from any of the sequences  
 CC from 30 lists given in the specification. Also disclosed is a method for  
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a  
 CC patient expressing a specific MHC class I allele by contacting cytotoxic  
 CC T cells from the patient with the composition cited above. The  
 CC composition comprises an epitope that is joined by an amino acid linker.  
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is  
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2  
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL  
 CC binds to a complex of the HLA molecule and the epitope. Specifically  
 CC claimed are peptides having allele-specific binding motifs for HLA. The  
 CC compositions and methods are useful for preventing, treating or  
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as  
 CC diagnostic agents for evaluating immune responses, for making antibodies  
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-  
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 2 AA;

Query Match 100.0%; Score 6; DB 7; Length 2;

Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
2 F 2

## RESULT 12

ADW36737  
ID ADW36737 standard; peptide; 2 AA.

XX AC ADW36737;  
XX DT 10-MAR-2005 (first entry)  
XX DE HLA binding epitope #7487.  
XX KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
XX KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
XX KW viral disease; cancer.

XX OS Unidentified.

XX PN WO2003040165-A2.

XX PD 15-MAY-2003.

XX PF 18-OCT-2001; 2001WO-US051650.

XX PR 19-OCT-2000; 2000US-0242350P.

XX PR 20-APR-2001; 2001US-0285624P.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S;

XX DR WPI; 2003-441519/41.

XX PT New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.

XX PS Claim 1; Page 52-379; 382pp; English.

XX CC The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically, claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251-ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX SQ Sequence 2 AA;

Query Match 100.0%; Score 6; DB 7; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
1 F 1

Db

## RESULT 13

ADW36731  
ID ADW36731 standard; peptide; 2 AA.

XX AC ADW36731;

XX DT 10-MAR-2005 (first entry)

XX DE HLA binding epitope #7481.

XX KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;  
XX KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;  
XX KW viral disease; cancer.

XX OS Unidentified.

XX PN WO2003040165-A2.

XX PD 15-MAY-2003.

XX PF 18-OCT-2001; 2001WO-US051650.

XX PR 19-OCT-2000; 2000US-0242350P.

XX PR 20-APR-2001; 2001US-0285624P.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S;

XX DR WPI; 2003-441519/41.

XX PT New composition comprising at least one peptide having allele-specific binding motifs for HLA, useful for preventing, treating or diagnosing viral diseases and cancer.

XX PS Claim 1; Page 52-379; 382pp; English.

XX CC The invention relates to a composition comprising at least one peptide having an isolated, prepared epitope selected from any of the sequences from 30 lists given in the specification. Also disclosed is a method for inducing a cytotoxic T cell response against a pre-selected antigen in a patient expressing a specific MHC class I allele by contacting cytotoxic T cells from the patient with the composition cited above. The composition comprises an epitope that is joined by an amino acid linker. The epitope is admixed or joined to a CTL or HTL epitope. The epitope is bound to an HLA molecule on the antigen-presenting cell, where when an A2-restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL binds to a complex of the HLA molecule and the epitope. Specifically, claimed are peptides having allele-specific binding motifs for HLA. The compositions and methods are useful for preventing, treating or diagnosing viral diseases and cancer. The peptide epitopes are useful as diagnostic agents for evaluating immune responses, for making antibodies and for evaluating efficacy of a vaccine. Sequences given in ADW29251-ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX SQ Sequence 2 AA;

Query Match 100.0%; Score 6; DB 7; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
1 F 1

Db

## RESULT 14

ADW36724  
ID ADW36724 standard; peptide; 2 AA.

XX AC ADW36724;

XX

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DT 10-MAR-2005 (first entry)
XX HLA binding epitope #7474.
DE
XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.
OS Unidentified.
XX WO2003040165-A2.
XX
XX 15-MAY-2003.
XX
XX 18-OCT-2001; 2001WO-US051650.
XX
XX 19-OCT-2000; 2000US-0242350P.
XX
XX 20-APR-2001; 2001US-0285624P.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S;
XX WPI; 2003-441519/41.
XX
XX New composition comprising at least one peptide having allele-specific
XX binding motifs for HLA, useful for preventing, treating or diagnosing
XX viral diseases and cancer.
XX
XX Claim 1; Page 52-379; 382pp; English.
XX
XX The invention relates to a composition comprising at least one peptide
XX having an isolated, prepared epitope selected from any of the sequences
XX from 30 lists given in the specification. Also disclosed is a method for
XX inducing a cytotoxic T cell response against a pre-selected antigen in a
XX patient expressing a specific MHC class I allele by contacting cytotoxic
XX T cells from the patient with the composition cited above. The
XX composition comprises an epitope that is joined by an amino acid linker.
XX The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
XX bound to an HLA molecule on the antigen-presenting cell, where when an A2
XX -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
XX binds to a complex of the HLA molecule and the epitope. Specifically
XX claimed are peptides having allele-specific binding motifs for HLA. The
XX compositions and methods are useful for preventing, treating or
XX diagnosing viral diseases and cancer. The peptide epitopes are useful as
XX diagnostic agents for evaluating immune responses, for making antibodies
XX and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
XX ADW37745 represent epitopes of the invention as given in Tables 2-31.
XX
XX Sequence 2 AA;
XX
XX Query Match 100.0%; Score 6; DB 7; Length 2;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 F 1
XX 1 F 1
XX
XX RESULT 15
XX ADW36734
XX ID ADW36734 standard; peptide; 2 AA.
XX
XX AC ADW36734;
XX
XX DT 10-MAR-2005 (first entry)
XX
XX HLA binding epitope #7484.
XX
XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
KW viral disease; cancer.

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XX OS Unidentified.
XX WO2003040165-A2.
XX
XX 15-MAY-2003.
XX
XX 18-OCT-2001; 2001WO-US051650.
XX
XX 19-OCT-2000; 2000US-0242350P.
XX
XX 20-APR-2001; 2001US-0285624P.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S;
XX WPI; 2003-441519/41.
XX
XX New composition comprising at least one peptide having allele-specific
XX binding motifs for HLA, useful for preventing, treating or diagnosing
XX viral diseases and cancer.
XX
XX Claim 1; Page 52-379; 382pp; English.
XX
XX The invention relates to a composition comprising at least one peptide
XX having an isolated, prepared epitope selected from any of the sequences
XX from 30 lists given in the specification. Also disclosed is a method for
XX inducing a cytotoxic T cell response against a pre-selected antigen in a
XX patient expressing a specific MHC class I allele by contacting cytotoxic
XX T cells from the patient with the composition cited above. The
XX composition comprises an epitope that is joined by an amino acid linker.
XX The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
XX bound to an HLA molecule on the antigen-presenting cell, where when an A2
XX -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
XX binds to a complex of the HLA molecule and the epitope. Specifically
XX claimed are peptides having allele-specific binding motifs for HLA. The
XX compositions and methods are useful for preventing, treating or
XX diagnosing viral diseases and cancer. The peptide epitopes are useful as
XX diagnostic agents for evaluating immune responses, for making antibodies
XX and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
XX ADW37745 represent epitopes of the invention as given in Tables 2-31.
XX
XX Sequence 2 AA;
XX
XX Query Match 100.0%; Score 6; DB 7; Length 2;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 F 1
XX 1 F 1
XX
XX RESULT 16
XX ADL77012
XX ID ADL77012 standard; peptide; 2 AA.
XX
XX AC ADL77012;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Albumin fusion protein related therapeutic protein X, SEQ ID No 494.
XX
XX albumin fusion protein; cytostatic; antianaemic; antiarthritic;
XX antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;
XX antipsoriatic; antibacterial; osteopathic; dermatological; antigout;
XX immunomodulator; antiarrhythmic; cardiac; nootropic; antilipaemic;
XX nephrotropic; uterine; neuroprotective; antiparkinsonian; tranquilizer;
XX antidiabetic; anabolic; hypertensive; vulnary; gene therapy; cancer;
XX reproductive system disorder; therapeutic protein.
XX
XX Unidentified.
XX

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PN US2004010134-A1.  
XX  
PD  
XX 15-JAN-2004.  
XX  
PF 12-APR-2001; 2001US-00833245.  
XX  
PR 12-APR-2000; 2000US-0229358P.  
PR 25-APR-2000; 2000US-0199384P.  
PR 21-DEC-2000; 2000US-0256931P.  
XX  
XX (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
XX  
XX Rosen CA, Haseltine WA;  
XX  
XX WPI; 2004-090519/09.  
XX  
XX New albumin fusion proteins, useful for diagnosing, treating, preventing  
PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,  
PT asthma, inflammatory bowel disease or Alzheimer's disease.  
XX  
XX Disclosure; SEQ ID NO 494; 279pp; English.  
XX  
XX The invention relates to a novel albumin fusion protein. The invention  
CC further relates to: a composition comprising the albumin fusion protein  
CC and a pharmaceutical carrier; a kit comprising the composition of the  
CC albumin fusion protein formula; a method of treating a disease or  
CC disorder in a patient comprising the step of administering the albumin  
CC fusion protein; a method of treating a patient with a disease or disorder  
CC that is modulated by Therapeutic protein: X, or its fragment or variant;  
CC a method of extending the shelf life of Therapeutic protein: X, or its  
CC fragment or variant; a nucleic acid molecule comprising a polynucleotide  
CC sequence encoding the albumin fusion protein; a vector comprising the  
CC nucleic acid molecule of the albumin fusion protein; and a host cell  
CC comprising the nucleic acid molecule of the albumin fusion protein. The  
CC albumin fusion protein and its compositions have the following  
CC activities: cytostatic, antianemic, antiarthritic, antiasthmatic, anti-  
CC HIV, immunosuppressive, antiinflammatory, antipapillary, antibacterial,  
CC osteopathic, dermatological, antitumor, immunomodulator, antiarrhythmic,  
CC cardiant, nontropic, antipapillary, nephrotropic, uropathic,  
CC neuroprotective, antipapillary, tranquilizer, antidiabetic, anabolic,  
CC hypertensive, and vulnerary. The albumin fusion protein is  
CC useful in gene therapy to treat disorders. The albumin fusion protein is  
CC useful for diagnosing, treating, preventing or ameliorating diseases or  
CC disorders comprising indication: Y. The diseases or disorders include:  
CC cancer (e.g. leukemia, colon, bone, breast, liver or lung cancer),  
CC immune or hematopoietic diseases (e.g. anemia, Hodgkin's disease, acute  
CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,  
CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme  
CC disease), reproductive system disorders (e.g. prostatitis, inguinal  
CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-  
CC Leydig tumors), musculoskeletal diseases (e.g. giant cell tumors,  
CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy  
CC or cachexia), cardiovascular disease (e.g. rhabdomyoma, heart disease,  
CC arrhythmia, cardiac arrest, heart valve disease, hypernatremia or  
CC hyponatremia), mixed foetal diseases (e.g. foetal alcohol syndrome,  
CC Down's syndrome, Fatau syndrome, Turner's syndrome, Apert syndrome or Tay  
CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary  
CC tract infections or renal disorders), neural or sensory disease (e.g.  
CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,  
CC cerebellar ataxia, attention deficit disorder, autism or obsessive  
CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or  
CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's  
CC disease or glomerulonephritis), digestive diseases (e.g. portal  
CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)  
CC or connective tissue or epithelial diseases (e.g. Crohn's disease,  
CC scleroderma, wound healing or epidermolysis bullosa). This sequence  
CC represents a therapeutic protein X relating to the albumin fusion protein  
CC of the invention. The sequence listing data for this specification was  
CC downloaded from the USPTO website.  
XX  
XX Sequence 2A;

Query Match 100.0%; Score 6; DB 8; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1  
RESULT 17  
ADL77640  
ID ADL77640 standard; peptide; 2 AA.  
XX  
XX AC ADL77640;  
XX  
XX DT 20-MAY-2004 (first entry)  
XX  
XX DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1122.  
XX  
XX KW albumin fusion protein; cytostatic; antianemic; antiarthritic;  
KW antiasthmatic; anti-HIV; immunosuppressive; antiinflammatory;  
KW antipapillary; antibacterial; osteopathic; dermatological; antitumor;  
KW immunomodulator; antiarrhythmic; cardiant; nephrotropic; antipapillary;  
KW nephrotropic; uropathic; neuroprotective; antipapillary; tranquilizer;  
KW antidiabetic; anabolic; hypertensive; vulnerary; gene therapy; cancer;  
KW reproductive system disorder; therapeutic protein.  
XX  
XX OS Unidentified.  
XX  
XX PN US2004010134-A1.  
XX  
XX PD 15-JAN-2004.  
XX  
XX PF 12-APR-2001; 2001US-00833245.  
XX  
XX PR 12-APR-2000; 2000US-0229358P.  
PR 25-APR-2000; 2000US-0199384P.  
PR 21-DEC-2000; 2000US-0256931P.  
XX  
XX (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
XX  
XX Rosen CA, Haseltine WA;  
XX  
XX WPI; 2004-090519/09.  
XX  
XX New albumin fusion proteins, useful for diagnosing, treating, preventing  
PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,  
PT asthma, inflammatory bowel disease or Alzheimer's disease.  
XX  
XX Disclosure; SEQ ID NO 1122; 279pp; English.  
XX  
XX The invention relates to a novel albumin fusion protein. The invention  
CC further relates to: a composition comprising the albumin fusion protein  
CC and a pharmaceutical carrier; a kit comprising the composition of the  
CC albumin fusion protein formula; a method of treating a disease or  
CC disorder in a patient comprising the step of administering the albumin  
CC fusion protein; a method of treating a patient with a disease or disorder  
CC that is modulated by Therapeutic protein: X, or its fragment or variant;  
CC a method of extending the shelf life of Therapeutic protein: X, or its  
CC fragment or variant; a nucleic acid molecule comprising a polynucleotide  
CC sequence encoding the albumin fusion protein; a vector comprising the  
CC nucleic acid molecule of the albumin fusion protein; and a host cell  
CC comprising the nucleic acid molecule of the albumin fusion protein. The  
CC albumin fusion protein and its compositions have the following  
CC activities: cytostatic, antianemic, antiarthritic, antiasthmatic, anti-  
CC HIV, immunosuppressive, antiinflammatory, antipapillary, antibacterial,  
CC osteopathic, dermatological, antitumor, immunomodulator, antiarrhythmic,  
CC cardiant, nontropic, antipapillary, nephrotropic, uropathic,  
CC neuroprotective, antipapillary, tranquilizer, antidiabetic, anabolic,  
CC hypertensive, and vulnerary. The albumin fusion protein is  
CC useful in gene therapy to treat disorders. The albumin fusion protein is  
CC useful for diagnosing, treating, preventing or ameliorating diseases or  
CC disorders comprising indication: Y. The diseases or disorders include:  
CC cancer (e.g. leukemia, colon, bone, breast, liver or lung cancer),  
CC immune or hematopoietic diseases (e.g. anemia, Hodgkin's disease, acute  
CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,  
CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme  
CC disease), reproductive system disorders (e.g. prostatitis, inguinal  
CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-  
CC Leydig tumors), musculoskeletal diseases (e.g. giant cell tumors,  
CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy  
CC or cachexia), cardiovascular disease (e.g. rhabdomyoma, heart disease,  
CC arrhythmia, cardiac arrest, heart valve disease, hypernatremia or  
CC hyponatremia), mixed foetal diseases (e.g. foetal alcohol syndrome,  
CC Down's syndrome, Fatau syndrome, Turner's syndrome, Apert syndrome or Tay  
CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary  
CC tract infections or renal disorders), neural or sensory disease (e.g.  
CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,  
CC cerebellar ataxia, attention deficit disorder, autism or obsessive  
CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or  
CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's  
CC disease or glomerulonephritis), digestive diseases (e.g. portal  
CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)  
CC or connective tissue or epithelial diseases (e.g. Crohn's disease,  
CC scleroderma, wound healing or epidermolysis bullosa). This sequence  
CC represents a therapeutic protein X relating to the albumin fusion protein  
CC of the invention. The sequence listing data for this specification was  
CC downloaded from the USPTO website.  
XX  
XX Sequence 2A;

disorders comprising indication: Y. The diseases or disorders include:  
 cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer),  
 immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute  
 lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,  
 autoimmune disease, inflammatory bowel disease, psoriasis or Lyme  
 disease), reproductive system disorders (e.g. prostatitis, inguinal  
 hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-  
 Leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,  
 Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy  
 or cachexia), cardiovascular disease (e.g. rhabdomyoma, heart disease,  
 arrhythmia), cardiac arrest, heat valve disease, hypernatraemia or  
 hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome,  
 Down's syndrome, Patau syndrome, Turner's syndrome, Apert syndrome or Tay  
 Sachs disease), excretory diseases (e.g. urinary incontinence, urinary  
 tract infections or renal disorders), neural or sensory disease (e.g.  
 Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,  
 cerebellar ataxia, attention deficit disorder, autism or obsessive  
 compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or  
 occupational lung disease), endocrine diseases (e.g. diabetes, Addison's  
 disease or glomerulonephritis), digestive diseases (e.g. portal  
 hypertension, irritable bowel disease, gastric atrophy or pancreatitis)  
 or connective tissue or epithelial diseases (e.g. Crohn's disease,  
 scleroderma, wound healing or epidermolysis bullosa). This sequence  
 represents a therapeutic protein X relating to the albumin fusion protein  
 of the inventor. The sequence listing data for this specification was  
 downloaded from the USPTO website.

XX SQ Sequence 2 AA;

Query Match 100.0%; Score 6; DB 8; Length 2;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

Db 2 F 2

RESULT 18

ADU07108

ID ADU07108 standard; peptide; 2 AA.

AC ADU07108;

XX 13-JAN-2005 (first entry)

DE Fungal growth inhibitor peptide #153.

XX fungicide; fungal growth inhibitor; peptidomimetic; antifungal;

KW anti-inflammatory; anti-microbial; fungal contamination.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..2 /note= "D-form residue"

FT Modified-site 1 /note= "Phe-2,3,4,5,6-F"

FT Modified-site 2 /note= "cyclohexylalanine"

XX WO2004089396-A2.

XX 21-OCT-2004.

XX 07-APR-2004; 2004WO-IB001523.

XX 07-APR-2003; 2003US-0461109P.

PR 05-APR-2004; 2004US-00819375.

XX (CANB-) CANBAS CO LTD.

XX Kawabe T, Kobayashi H,

XX

DR

XX

PT

PT

XX

PS

XX

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WPI; 2004-757842/74.

Composition useful for treating fungal infections e.g. black spot  
 comprises peptide or peptidomimetic, and optionally another agents having  
 antifungal activity, and anti-inflammatory or anti-microbial agents.

Disclosure; SEQ ID NO 153; 58pp; English.

The invention relates to a composition comprising a peptide or  
 peptidomimetic, and optionally another agents having antifungal activity,  
 or one of anti-inflammatory or anti-microbial agents. The peptide or  
 peptidomimetic has a sequence, which is at least 90% identical to a  
 sequence P1-P2-P3-P4-P5-P6, P6-P5-P4-P3-P2-P1 or their prodrugs where P1  
 = d- or l-Cha; d- or l-Nal(2); d- or l-(Phe-2,3,4,5,6-F); d- or l-(Phe-  
 3,4,5-F); d- or l-(Phe-4CF3); an amino acid that occupies a similar side  
 chain space; or T1; T1 = an amino acid with 1-2 aromatic, piperidine,  
 pyrazine, pyrimidine, piperazine, morpholine or pyrimidine group(s); or  
 one indole, pentylene, indene, naphthalene group, benzofuran,  
 benzothioephene, quinoline, indoline, chroman, quinoxaline or quinoxaline  
 group in the side chain; P2 = d- or l-Cha, d- or l-Nal(2), d- or l-(Phe-  
 2,3,4,5,6-F), d- or l-(Phe-3,4,5-F), d- or l-(Phe-4-CF 3 ), d- or l-Bpa,  
 d- or l-Phe-4-NO 2 , an amino acid that occupies a similar side chain  
 space; or T1; P3-P5 = amino acid or a carbon chain such that the distance  
 between P2 and P6 is about the same as the distance when each of P3-P5  
 are amino acids; P6 = d- or l-Bpa, d- or l-Phe-4-NO 2 , amino acid and d-  
 or l-Tyr, amino acid and d- or l-Phe, any amino acid or absent. The  
 compound is useful for inhibiting or reducing fungal infection or fungal  
 growth, fungal contamination (by e.g. yeast, mold, slimes, such as  
 Candida, Saccharomyces, dermatophytes, Coccidioides immitis, such as  
 Histoplasma capsulatum, Candida albicans and Aspergillus fumigatus ) in  
 human and plant (including cultured cells), non-living object (e.g.  
 inorganic material and organic chemistry) in the environment, in a  
 residential, commercial, industrial or community setting, or in an  
 agricultural or horticultural setting; and for treating disorders and  
 conditions associated with fungus e.g. onychomycosis, Jock-itch or  
 athlete's foot, paracoccidioidomycosis, blastomycosis, mucormycosis,  
 cryptococcosis, coccidioidomycosis, histoplasmosis, candidiasis,  
 aspergillosis, black spot, glomerella, ripe spot, sooty blotch, septoria  
 leaf spot, cercospora leaf spot, rust, downy mildew, brown rot, brown  
 patch, a smut, verrucosia, dead arm disease, mycosphaerella leafspot,  
 black spot (roses), flower blight, early and late blight, leaf mould,  
 anthracnose, ring spot, dollar spot, northern leafblight, alternaria and  
 lespora spot. The peptides and the peptidomimetics exhibit excellent  
 antifungal activity, hence the composition reduces various symptoms  
 associated with the fungal infection such as irritation, itching,  
 inflammation, burning, hives, weeping, pruritus, excess discharge,  
 discoloration, headache, fatigue and susceptibility to or recurrence of  
 fungal growth or fungal infection; and inhibits worsening or progression  
 of the patient's condition. This sequence corresponds to an example of  
 the peptide or peptidomimetic of the invention.

Sequence 2 AA;

Query Match 100.0%; Score 6; DB 8; Length 2;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

Db 1 F 1

RESULT 19

AAP20375

ID AAP20375 standard; protein; 3 AA.

XX

AC AAP20375;

XX

DT 27-NOV-1992 (first entry)

XX

DE Analgesic peptide #7 binds morphine receptors.

XX



PT hypertension and hyperaldosteronism.  
XX  
PS Claim 1; Page 63; 64pp; English.  
XX  
CC This peptide is used to treat renin-associated hypertension and  
CC hyperaldosteronism. When used as a renin inhibitor the daily dose is  
CC pref. 25-750 mg of body weight. See also AAR2691-P82708 and AAR2710-  
CC P82713. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 3 AA;  
Query Match 100.0%; Score 6; DB 1; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1  
1 F 1  
1 F 1  
RESULT 22  
AAR29096  
ID AAR29096 standard; peptide; 3 AA.  
XX  
AC AAR29096;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-APR-1993 (first entry)  
XX  
DE Cathepsin G inhibiting fragment.  
XX  
KW Cathepsin G; elastase; connective tissue; degradation; protease; gout;  
KW rheumatoid arthritis; emphysema; ARDS;  
KW adult respiratory distress syndrome; para-phenylene.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "N-terminal amino acids of the peptides of  
FT AAR29095-96 are linked by -C(O)-para-phenylene-C(O)-"  
FT Modified-site 4  
FT /note= "C-terminal Phe is in keto form, i.e. OH replaced  
FT by CF3"  
FT  
FT  
FT  
PN WO9220357-A1.  
XX  
XX 26-NOV-1992.  
XX  
PF 21-APR-1992; 92WO-US003288.  
XX  
PR 23-MAY-1991; 91US-00704499.  
XX  
PA (RICH ) MERRELL DOW PHARM INC.  
XX  
PI Angelastro MR, Bey P, Doherty NS, Janusz MJ, Mehdi S, Peet NP;  
XX WPI; 1992-415461/50.  
XX  
XX New peptide derivs. used as cathepsin G and elastase inhibitors - for  
PT treating gout, rheumatoid arthritis, inflammatory disorders, emphysema  
PT and adult respiratory distress syndrome.  
XX  
PS Claim 18; Page 53; 53pp; English.  
XX  
CC Inhibitors of cathepsin G and elastase for preventing connective tissue  
CC degradation are chemically linked inhibitors of the proteases elastase  
CC (AAR29095) and cathepsin G (AAR29096). The N-terminal amino acids of the  
CC peptides of AAR29095-96 are linked by -C(O)-para-phenylene-C(O)-. The cpd.  
CC has an anti-inflammatory effect useful in the treatment of gout,  
CC rheumatoid arthritis and other inflammatory diseases and to prevent  
CC elastin mediated tissue damage. It can also be used in the treatment of  
CC emphysema and adult respiratory distress syndrome. (Updated on 25-MAR-

CC 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 3 AA;  
Query Match 100.0%; Score 6; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 3 F 3  
1 F 1  
3 F 3  
RESULT 23  
AAR38411  
ID AAR38411 standard; protein; 3 AA.  
XX  
AC AAR38411;  
XX  
DT 29-OCT-1993 (first entry)  
XX  
DE Cathepsin G inhibitor peptide #2.  
XX  
KW Inflammatory disease; prevention; rheumatoid arthritis; emphysema;  
KW neutrophil-mediated connective tissue degradation; gout; elastase;  
KW inhibition; adult respiratory distress syndrome.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /note= "Linked via a linking chain such as -CO-phenylene-  
FT CO- to the N-terminal of a Cathepsin G inhibiting  
FT molecule as described in AAR38410-11"  
FT Modified-site 4  
FT /note= "May opt. be modified by COCOR, CF2CF3, CF3, CHF2,  
FT COOR3, CONHR3, CF2CHR3CONHR, H, alkyl, aryl, aralkyl or  
FT COR; where R3 is H, alkyl, phenyl or benzyl and R is OH  
FT or alkoxy"  
FT  
FT  
FT  
PN ZA9203602-A.  
XX  
PD 24-FEB-1993.  
XX  
PF 18-MAY-1992; 92ZA-00003602.  
XX  
PR 23-MAY-1991; 91US-00704499.  
XX  
PA (RICH ) MERRELL DOW PHARM INC.  
XX  
PI Angelastro MM, Bey P, Doherty NS, Janusz MJ, Mehdi S, Peet NP;  
XX WPI; 1992-415461/50.  
XX  
XX New peptide derivs. used as cathepsin G and elastase inhibitors - for  
PT treating gout, rheumatoid arthritis, inflammatory disorders, emphysema  
PT and adult respiratory distress syndrome.  
XX  
PS Claim 13-17; Page 52; 55pp; English.  
XX  
CC The sequences given in AAR38410-11 are cathepsin G inhibiting peptides  
CC which were produced by standard peptide synthesis methods. In the context  
CC of the invention one of these peptides may be linked via their N-termini  
CC to an elastase inhibiting peptide (see features table). The peptide  
CC conjugates may be used to prevent neutrophil-mediated connective tissue  
CC degradation associated with inflammatory diseases eg. gout and rheumatoid  
CC arthritis. They may also be used for preventing elastin-mediated tissue  
CC damage in the treatment of emphysema and adult respiratory distress  
CC syndrome  
XX  
SQ Sequence 3 AA;  
Query Match 100.0%; Score 6; DB 2; Length 3;



Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 24  
AAR39998  
ID AAR39998 standard; peptide; 3 AA.  
XX  
AC AAR39998;  
XX  
DT 25-MAR-2003 (revised)  
DT 23-MAY-1994 (first entry)  
XX  
XX Scintigraph imaging agent specific binding peptide.  
XX  
XX Reagent; site imaging; technetium-99m labelled; peptide.  
KW  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 2 .3  
FT Modified-site 3  
FT /note= "peptide bond replaced by CO-CH2-N"  
FT /label= OTHER  
FT /note= "Diq (decahydroisoquinoline carboxylic acid) which  
FT is in C-terminal t-butylamide form"  
XX  
PN WO9301828-A1.  
XX  
XX 04-FEB-1993.  
XX  
XX 22-JUL-1992; 92WO-US006153.  
PF  
XX 23-JUL-1991; 91US-00734434.  
PR  
XX (VICA-) VICAL INC.  
PA  
XX Basava C, Hostetler KY;  
PI  
XX WPI; 1993-058523/07.  
DR  
XX New peptide(s) and lipid conjugates - useful as protease inhibitors for  
XX treating viral infections, e.g. HIV and associated conditions e.g. AIDS  
XX and ARC.  
XX  
XX Claim 1; Page 62; 72pp; English.  
XX  
XX The invention relates to peptide-lipid linking structures (the lipids are  
XX phospholipids, glycerides or other membrane-targeting or -anchoring  
XX species), and also to new HIV protease inhibitors (of which the present  
XX sequence is one). The compounds possess activity against viral infection  
XX and inhibitory activity towards viral proteases. They are useful in the  
XX prophylaxis and treatment of viral infections, particularly HIV and ARC.  
XX The linked structures may also be useful for delivering other protease  
XX inhibitors, particularly renin inhibitors useful in treatment of  
XX hypertension. The linked peptides are suitable for administration in  
XX liposome form. Conjugation of the peptides to lipids increases the plasma  
XX half life and protects against tissue and renal clearance. The conjugates  
XX can survive to be delivered to macrophages, a major HIV infection site.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 3 AA;  
Query Match 100.0%; Score 6; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 25  
AAR59333  
ID AAR59333 standard; peptide; 3 AA.  
XX  
AC AAR59333;  
XX  
XX 25-MAR-2003 (revised)  
DT 29-JUL-1994 (first entry)  
XX

DE HIV protease inhibiting peptide.  
XX  
KW HIV; protease inhibitor; antiviral; AIDS; ARC; liposome; lipid;  
KW conjugate; linker; phospholipid; glyceride; enzyme; renin; hypertension.  
XX  
OS Synthetic.  
XX  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 2 .3  
FT Modified-site 3  
FT /note= "peptide bond replaced by CO-CH2-N"  
FT /label= OTHER  
FT /note= "Diq (decahydroisoquinoline carboxylic acid) which  
FT is in C-terminal t-butylamide form"  
XX  
PN WO9301828-A1.  
XX  
XX 04-FEB-1993.  
XX  
XX 22-JUL-1992; 92WO-US006153.  
PF  
XX 23-JUL-1991; 91US-00734434.  
PR  
XX (VICA-) VICAL INC.  
PA  
XX Basava C, Hostetler KY;  
PI  
XX WPI; 1993-058523/07.  
DR  
XX New peptide(s) and lipid conjugates - useful as protease inhibitors for  
XX treating viral infections, e.g. HIV and associated conditions e.g. AIDS  
XX and ARC.  
XX  
XX Claim 1; Page 62; 72pp; English.  
XX  
XX The invention relates to peptide-lipid linking structures (the lipids are  
XX phospholipids, glycerides or other membrane-targeting or -anchoring  
XX species), and also to new HIV protease inhibitors (of which the present  
XX sequence is one). The compounds possess activity against viral infection  
XX and inhibitory activity towards viral proteases. They are useful in the  
XX prophylaxis and treatment of viral infections, particularly HIV and ARC.  
XX The linked structures may also be useful for delivering other protease  
XX inhibitors, particularly renin inhibitors useful in treatment of  
XX hypertension. The linked peptides are suitable for administration in  
XX liposome form. Conjugation of the peptides to lipids increases the plasma  
XX half life and protects against tissue and renal clearance. The conjugates  
XX can survive to be delivered to macrophages, a major HIV infection site.  
XX (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 3 AA;  
Query Match 100.0%; Score 6; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 26  
AAR47530  
ID AAR47530 standard; peptide; 3 AA.  
XX  
AC AAR47530;  
XX  
XX 25-MAR-2003 (revised)  
DT 20-JUN-1994 (first entry)  
XX  
XX GHRP-6 analog.  
DE

KW GHRP-6 analog; growth hormone releasing compound; somatoliberein;  
 KW somatotropin.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Misc-difference 1 /note= "D-form residue"  
 FT  
 FT Misc-difference 2 /note= "D-form residue"  
 FT  
 FT Modified-site 3  
 FT /note= "C-terminal amide"  
 XX  
 XX

PN WO9400759-A1.

XX 06-JAN-1994.

XX 22-JUN-1993; 93WO-US005955.

XX 29-JUN-1992; 92US-00905760.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Bercu BB, Walker RF;

XX WPI; 1994-026357/03.

XX Establishing aetiology of short stature in children - by measuring growth  
 PT hormone levels after admin. of growth hormone releasing cpd., peptide  
 PT GHRP-6 or both.

XX Claim 3; Page 12; 18pp; English.

XX GHRP-6 analogs given in AAR47523-35 stimulate release of human growth  
 CC hormone by the same mechanism as GHRP-6. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

XX Sequence 3 AA;

Query Match 100.0%; Score 6; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

Db 3 F 3

RESULT 27

AAR47853

ID AAR47853 standard; peptide; 3 AA.

XX AAR47853;

XX 25-MAR-2003 (revised)

DT 22-JUN-1994 (first entry)

XX Calpain inhibitor.

XX Cell reproduction; dividing cells; GI stage; chemotherapy; cancer;  
 KW neurodegeneration; Alzheimer's disease; ischaemia; subarachnoid;  
 KW haemorrhage.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "MeO-Suc-Val"

FT Misc-difference 3 /note= "DL-Phe-CO2Me"

FT WO9400095-A2.

XX

PD 06-JAN-1994.

XX 24-JUN-1993; 93WO-US006143.

XX 24-JUN-1992; 92US-00903800.

PR 16-MAR-1993; 93US-00034996.

PR 01-JUN-1993; 93US-00072609.

XX (CORT-) CORTEX PHARM INC.

PA (GEOR-) GEORGIA TECH RES CORP.

XX Eveleth DD, Lynch G, Powers JC, Bartus RT;

XX WPI; 1994-025846/03.

XX Blocking actively dividing cells in GI stage using calpain inhibitor -  
 PT esp. to increase efficiency of cancer chemotherapy and cell  
 PT transformation, inhibitors also useful for treating e.g. muscle damage,  
 PT cataract, vasospasm etc.

XX Example PKC10; Page 103; 258pp; English.

XX The compound is an example of a calpain inhibitor which may be used to  
 CC synchronise the reproductive cycle in actively reproducing cells, by  
 CC blocking cell progression from the G1 to S phase. This synchronisation is  
 CC used to shorten the duration of chemotherapy of cancer and to increase  
 CC activity of the chemotherapeutic agent and to increase the efficiency of  
 CC cell transformation or integration of foreign DNA into cells. Activation  
 CC by calpain is an early event leading to cell death and damage, so the  
 CC cpd. may be used to treat such cells before extensive damage occurs, e.g.  
 CC to treat neurodegeneration in ischaemia, subarachnoid haemorrhage and  
 CC Alzheimer's disease. AAR47852-4. (Updated on 25-MAR-2003 to correct PN  
 CC field.)

XX Sequence 3 AA;

Query Match 100.0%; Score 6; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

Db 3 F 3

RESULT 28

AAR53239

ID AAR53239 standard; peptide; 3 AA.

XX AAR53239;

XX 05-DEC-1994 (first entry)

XX Heparin derivative peptide #3.

XX Substitution; amino position; heparin; derivative; denitrified;  
 KW sulphated; acetylated; translatability; tumour; drug release; support;  
 KW side effects.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "-OH, -H, or a protective group"

FT

XX JP06080705-A.

XX 22-MAR-1994.

XX 02-SEP-1992; 92JP-00234846.

XX 02-SEP-1992; 92JP-00234846.

XX

PA (DDSK-) DDS KENYUSHO KK.  
 XX WPI; 1994-132048/16.  
 DR  
 XX Heparin derivs having good translatability to tumour etc - consists of de  
 PT -nitrified and sulphated heparin with part of amino gps introduced with a  
 PT peptide chain(s) and the remaining amino gps acetylated.  
 XX  
 PS Claim 3; Page 2; 11pp; Japanese.  
 XX  
 CC The sequences given in AAR53237-43 are peptide chains which may be  
 CC substituted on to the amino position of a heparin derivative. The heparin  
 CC derivative consists of denitrified and sulphated heparin with on of these  
 CC peptides substituted on to an amino group and the remaining amino groups  
 CC being acetylated. The heparin derivatives have high translatability to  
 CC tumours and release drugs well in tumours. The complexes can support  
 CC drugs and can therefore deliver them to efficiently to tumours without  
 CC adverse side effects in other organs and allows use of drugs with  
 CC limitations in exerting medical effects in tumours  
 XX  
 SQ Sequence 3 AA;  
 Query Match 100.0%; Score 6; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 1 F 1  
 RESULT 29  
 AAR63264  
 ID AAR63264 standard; peptide; 3 AA.  
 XX  
 AC AAR63264;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-JUL-1995 (first entry)  
 XX  
 DE Thrombin inhibitor peptide, CSAP.  
 XX  
 KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;  
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation;  
 KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D form residue"  
 FT Modified-site 3  
 FT /note= "opt. modified with -H to give ALD, or CH2Cl to  
 FT give CMK"  
 XX  
 PN WO9425491-A1.  
 XX  
 XX 10-NOV-1994.  
 XX  
 XX 03-MAY-1994; 94WO-US0004881.  
 XX  
 XX 03-MAY-1993; 93US-00058699.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 XX (UYEM-) UNIV EMORY.  
 XX  
 XX Haber E, Bode C, Runge M;  
 XX WPI; 1994-358195/44.  
 XX  
 XX Fibrin-binding antibody linked to thrombin inhibitor - useful for  
 PT preventing blood coagulation by specifically targeting inhibitor to site  
 PT of thrombin activity.

XX Claim 7; Page 38; 53pp; English.  
 PS  
 XX This sequence represents an inhibitor of thrombin which was used in the  
 CC chimeric molecule of the invention. The chimeric molecule further  
 CC comprises a fibrin-binding antibody linked to the thrombin inhibitor  
 CC through a covalent linkage. The chimeric molecule allows fibrin-specific  
 CC antibody targeting of hirudin and other thrombin inhibitors, which is  
 CC more potent than thrombin on its own. The fibrin-specific antibody is  
 CC pref. the monoclonal antibody, 59D8. The epitope to which 59D8 binds  
 CC becomes available only after thrombin cleaves fibrinopeptide B. The  
 CC chimeric protein may be used for preventing coagulation of the blood.  
 CC Anti-thrombin targeting can be esp. useful in highly thrombogenic  
 CC situations such as coronary stent implantation and can be used as an  
 CC adjunctive therapy with highly selective thrombolytic agents. The  
 CC thrombin inhibitor is localised to sites of thrombin activity by the  
 CC antibody which binds to thrombin but does not cross react with uncleaved  
 CC fibrinogen. The selectivity of inhibition allows te total amount of  
 CC thrombin inhibitor used to be substantially reduced, resulting in a  
 CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003  
 CC to correct PN field.)  
 XX  
 SQ Sequence 3 AA;  
 Query Match 100.0%; Score 6; DB 2; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 1 F 1  
 RESULT 30  
 AAR63263  
 ID AAR63263 standard; peptide; 3 AA.  
 XX  
 AC AAR63263;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-JUL-1995 (first entry)  
 XX  
 DE Thrombin inhibitor peptide #4.  
 XX  
 KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;  
 KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation;  
 KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /label= H-(D)-Phe  
 FT Modified-site 3  
 FT /note= "boroArg-ClOH16"  
 XX  
 PN WO9425491-A1.  
 XX  
 XX 10-NOV-1994.  
 XX  
 XX 03-MAY-1994; 94WO-US0004881.  
 XX  
 XX 03-MAY-1993; 93US-00058699.  
 XX  
 XX (HARD ) HARVARD COLLEGE.  
 XX (UYEM-) UNIV EMORY.  
 XX  
 XX Haber E, Bode C, Runge M;  
 XX WPI; 1994-358195/44.  
 XX  
 XX Fibrin-binding antibody linked to thrombin inhibitor - useful for  
 PT preventing blood coagulation by specifically targeting inhibitor to site  
 PT of thrombin activity.

```

PT of thrombin activity.
XX Claim 7; Page 38; 53pp; English.
XX This sequence represents an inhibitor of thrombin which was used in the
CC chimeric molecule of the invention. The chimeric molecule further
CC comprises a fibrin-binding antibody linked to the thrombin inhibitor
CC through a covalent linkage. The chimeric molecule allows fibrin-specific
CC antibody targeting of hirudin and other thrombin inhibitors, which is
CC more potent than thrombin on its own. The fibrin-specific antibody is
CC pref. the monoclonal antibody, 59D8. The epitope to which 59D8 binds
CC becomes available only after thrombin cleaves fibrinopeptide B. The
CC chimeric protein may be used for preventing coagulation of the blood.
CC Anti-thrombin targeting can be esp. useful in highly thrombogenic
CC situations such as coronary stent implantation and can be used as an
CC adjunctive therapy with highly selective thrombolytic agents. The
CC thrombin inhibitor is localised to sites of thrombin activity by the
CC antibody which binds to thrombin but does not cross react with uncleaved
CC fibrinogen. The selectivity of inhibition allows te total amount of
CC thrombin inhibitor used to be substantially reduced, resulting in a
CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003
CC to correct PN field.)
XX Sequence 3 AA;
SQ
Query Match 100.0%; Score 6; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
DB 1 F 1
RESULT 31
AAR63261
ID AAR63261 standard; peptide; 3 AA.
XX AAR63261;
XX 25-MAR-2003 (revised)
DT 21-JUL-1995 (first entry)
XX Thrombin inhibitor peptide #2.
XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation;
KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /label= Boc-(D)-Phe
FT Modified-site 3 /note= "boroArg-C10H16"
FT Modified-site 3
XX WO9425491-A1.
XX 10-NOV-1994.
XX 03-MAY-1994; 94WO-US004881.
XX 03-MAY-1993; 93US-00058699.
XX (HARD ) HARVARD COLLEGE.
PA (UYEM-) UNIV EMORY.
XX Haber E, Bode C, Runge M;
XX WPI; 1994-358195/44.
XX Fibrin-binding antibody linked to thrombin inhibitor - useful for
preventing blood coagulation by specifically targetting inhibitor to site
of thrombin activity.
XX Claim 7; Page 38; 53pp; English.
XX This sequence represents an inhibitor of thrombin which was used in the
CC chimeric molecule of the invention. The chimeric molecule further
CC comprises a fibrin-binding antibody linked to the thrombin inhibitor
CC through a covalent linkage. The chimeric molecule allows fibrin-specific
CC antibody targeting of hirudin and other thrombin inhibitors, which is
CC more potent than thrombin on its own. The fibrin-specific antibody is
CC pref. the monoclonal antibody, 59D8. The epitope to which 59D8 binds
CC becomes available only after thrombin cleaves fibrinopeptide B. The
CC chimeric protein may be used for preventing coagulation of the blood.
CC Anti-thrombin targeting can be esp. useful in highly thrombogenic
CC situations such as coronary stent implantation and can be used as an
CC adjunctive therapy with highly selective thrombolytic agents. The
CC thrombin inhibitor is localised to sites of thrombin activity by the
CC antibody which binds to thrombin but does not cross react with uncleaved
CC fibrinogen. The selectivity of inhibition allows te total amount of
CC thrombin inhibitor used to be substantially reduced, resulting in a
CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003
CC to correct PN field.)
XX Sequence 3 AA;
SQ
Query Match 100.0%; Score 6; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
DB 1 F 1
RESULT 32
AAR63260
ID AAR63260 standard; peptide; 3 AA.
XX AAR63260;
XX 25-MAR-2003 (revised)
DT 21-JUL-1995 (first entry)
XX Thrombin inhibitor peptide #1.
XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation;
KW coronary stent implantation; adjunctive therapy; fibrinogen;
KW haemorrhaging.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /label= Ac-(D)-Phe
FT Modified-site 3 /note= "boroArg"
FT Modified-site 3
XX WO9425491-A1.
XX 10-NOV-1994.
XX 03-MAY-1994; 94WO-US004881.
XX 03-MAY-1993; 93US-00058699.
XX (HARD ) HARVARD COLLEGE.
PA (UYEM-) UNIV EMORY.
XX Haber E, Bode C, Runge M;
XX WPI; 1994-358195/44.

```

XX Fibrin-binding antibody linked to thrombin inhibitor - useful for  
PT preventing blood coagulation by specifically targeting inhibitor to site  
PT of thrombin activity.  
XX  
XX  
XX Claim 7; Page 38; 53pp; English.  
XX  
XX This sequence represents an inhibitor of thrombin which was used in the  
CC chimeric molecule of the invention. The chimeric molecule further  
CC comprises a fibrin-binding antibody linked to the thrombin inhibitor  
CC through a covalent linkage. The chimeric molecule allows fibrin-specific  
CC antibody targeting of hirudin and other thrombin inhibitors, which is  
CC more potent than thrombin on its own. The fibrin-specific antibody is  
CC pref. the monoclonal antibody, 59D8. The epitope to which 59D8 binds  
CC becomes available only after thrombin cleaves fibrinopeptide B. The  
CC chimeric protein may be used for preventing coagulation of the blood.  
CC Anti-thrombin targeting can be esp. useful in highly thrombogenic  
CC situations such as coronary stent implantation and can be used as an  
CC adjunctive therapy with highly selective thrombolytic agents. The  
CC thrombin inhibitor is localised to sites of thrombin activity by the  
CC antibody which binds to thrombin but does not cross react with uncleaved  
CC fibrinogen. The selectivity of inhibition allows te total amount of  
CC thrombin inhibitor used to be substantially reduced, resulting in a  
CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003  
CC to correct PN field.)  
XX  
XX Sequence 3 AA;  
SQ

Query Match 100.0%; Score 6; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1

RESULT 33  
AAR63262  
ID AAR63262 standard; peptide; 3 AA.  
AC  
XX AAR63262;  
XX  
XX 25-MAR-2003 (revised)  
DT 21-JUL-1995 (first entry)  
DT  
XX Thrombin inhibitor peptide #3.  
DE  
XX  
XX Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;  
KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation;  
KW coronary stent implantation; adjunctive therapy; fibrinogen; haemorrhage.  
XX  
XX Synthetic.  
OS  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /label= H-(D)-Phe  
FT Modified-site 3  
FT /note= "boroArg-OH"  
FT  
XX WO9425491-A1.  
XX  
XX 10-NOV-1994.  
PD  
XX  
XX 03-MAY-1994; 94WO-US004881.  
XX  
XX 03-MAY-1993; 93US-00058699.  
XX  
XX (HARD ) HARVARD COLLEGE.  
PA (UYEM-) UNIV EMORY.  
XX  
XX Haber E, Bode C, Runge M;  
XX

DR WPI; 1994-358195/44.  
XX  
XX Fibrin-binding antibody linked to thrombin inhibitor - useful for  
PT preventing blood coagulation by specifically targeting inhibitor to site  
PT of thrombin activity.  
XX  
XX Claim 7; Page 38; 53pp; English.  
XX  
XX This sequence represents an inhibitor of thrombin which was used in the  
CC chimeric molecule of the invention. The chimeric molecule further  
CC comprises a fibrin-binding antibody linked to the thrombin inhibitor  
CC through a covalent linkage. The chimeric molecule allows fibrin-specific  
CC antibody targeting of hirudin and other thrombin inhibitors, which is  
CC more potent than thrombin on its own. The fibrin-specific antibody is  
CC pref. the monoclonal antibody, 59D8. The epitope to which 59D8 binds  
CC becomes available only after thrombin cleaves fibrinopeptide B. The  
CC chimeric protein may be used for preventing coagulation of the blood.  
CC Anti-thrombin targeting can be esp. useful in highly thrombogenic  
CC situations such as coronary stent implantation and can be used as an  
CC adjunctive therapy with highly selective thrombolytic agents. The  
CC thrombin inhibitor is localised to sites of thrombin activity by the  
CC antibody which binds to thrombin but does not cross react with uncleaved  
CC fibrinogen. The selectivity of inhibition allows te total amount of  
CC thrombin inhibitor used to be substantially reduced, resulting in a  
CC reduced potential for generalised haemorrhaging. (Updated on 25-MAR-2003  
CC to correct PN field.)  
XX  
XX Sequence 3 AA;  
SQ

Query Match 100.0%; Score 6; DB 2; Length 3;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1

RESULT 34  
AAR47430  
ID AAR47430 standard; peptide; 3 AA.  
AC  
XX AAR47430;  
XX  
XX 27-AUG-2003 (revised)  
DT 30-JUN-1994 (first entry)  
DT  
XX ACE inhibiting peptide #1.  
DE  
XX  
XX Angiotensin I converting enzyme; ACE; inhibiting peptide; bonito; fish;  
KW hypertension; cerebral haemorrhage; cerebral infarction; eardine; head;  
KW subarachnoid haemorrhage; angina pectoris; myocardial infarction; tuna;  
KW nephrosclerosis; renal insufficiency; retinal venous occlusion;  
KW internal organs.  
XX  
XX Katsuwonus pelamis.  
OS  
XX  
XX JP05306296-A.  
XX  
XX 19-NOV-1993.  
PD  
XX  
XX 24-APR-1992; 92JP-00129817.  
XX  
XX 24-APR-1992; 92JP-00129817.  
XX  
XX (MARI-) ZH MARINO FORUM 21.  
XX  
XX WPI; 1994-002154/01.  
XX  
XX New tri- and tetra-peptide of fish origin - which inhibits angiotensin I  
PT converting enzyme, useful for treating circulation disorders including  
XX cerebral or myocardial infarction, nephrosclerosis, etc.  
XX

```

PS Claim 1; Page 2; 5pp; Japanese.
XX
CC The sequences given in AAR47430-31 are angiotensin I converting enzyme
CC (ACE) inhibiting peptides. GHF inhibits ACE by 50% at 1100 microm and
CC YRPV at 380 microm. They can be used in the treatment of hypertension and
CC its complications, eg. cerebral haemorrhage, cerebral infarction,
CC subarachnoid haemorrhage, angina pectoris, myocardial infarction,
CC nephrosclerosis, renal insufficiency and retinal venous occlusion. These
CC peptides were isolated from the head or internal organs of fish (eg.
CC bonito, sardine or tuna) by autolysis or they may be chemically
CC synthesised by a solid or liquid phase method. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
XX Sequence 3 AA;
XX
    Query Match      100.0%; Score 6; DB 2; Length 3;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 3 F 3

RESULT 35
AAR61093
ID AAR61093 standard; peptide; 3 AA.
XX
AC AAR61093;
XX
DT 21-MAY-1995 (first entry)
XX
DE ACE-inhibiting tripeptide.
XX
KW ACE; angiotensin converting enzyme inhibitor; fish meat alpha-1000;
KW hypotensive.
XX
OS Synthetic.
XX
XX JP06166697-A.
XX
XX 14-JUN-1994.
XX
XX 01-DEC-1992; 92JP-00343573.
XX
XX 01-DEC-1992; 92JP-00343573.
XX
XX (SENN-) SENMI EKESU KK.
XX
XX WPI; 1994-230661/28.
XX
XX New ACE-inhibiting di-, tri- and tetra:peptide(s) - obtd. by treating
XX fish meat alpha-1000 peptide with ODS resin.
XX
XX Claim 1; Page 2; 10pp; Japanese.
XX
CC A total of ten di-, tri- or tetrapeptides are claimed which have
CC angiotensin converting enzyme inhibiting activity and which are useful as
CC hypotensives. The present sequence is one of the ten. The peptides are
CC obtained by treating fish meat alpha-1000 peptide with ODS resin. This
CC peptide has an ACE inhibiting IC50 value of 330 micromolar
XX
XX Sequence 3 AA;
XX
    Query Match      100.0%; Score 6; DB 2; Length 3;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 2 F 2

```

```

RESULT 36
AAR58581
ID AAR58581 standard; peptide; 3 AA.
XX
AC AAR58581;
XX
DT 26-APR-1995 (first entry)
XX
DE Angiotensin I converting enzyme inhibitory tripeptide PKY.
XX
KW angiotensin converting enzyme; inhibitor; food ingredient.
XX
OS Synthetic.
XX
XX JP06220088-A.
XX
XX 09-AUG-1994.
XX
XX 22-JAN-1993; 93JP-00025977.
XX
XX 22-JAN-1993; 93JP-00025977.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
XX WPI; 1994-290911/36.
XX
XX New tri:peptide(s) - inhibit angiotensin I converting enzyme.
XX
XX Claim 1; Page 2; 4pp; Japanese.
XX
CC This is one of thirteen claimed tripeptides (AAR58569-R58581) which
CC inhibit angiotensin I converting enzyme (with IC50 of 2.9-186.2
CC micromolar). The tripeptides are incorporated into food, e.g. hamburgers
XX
XX Sequence 3 AA;
XX
    Query Match      100.0%; Score 6; DB 2; Length 3;
    Best Local Similarity 100.0%; Pred. No. 1.8e+06;
    Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 F 1
DB 1 F 1

RESULT 37
AAR58575
ID AAR58575 standard; peptide; 3 AA.
XX
AC AAR58575;
XX
XX 26-APR-1995 (first entry)
XX
XX Angiotensin I converting enzyme inhibitory tripeptide FRP.
XX
XX angiotensin converting enzyme; inhibitor; food ingredient.
XX
XX Synthetic.
XX
XX JP06220088-A.
XX
XX 09-AUG-1994.
XX
XX 22-JAN-1993; 93JP-00025977.
XX
XX 22-JAN-1993; 93JP-00025977.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
XX WPI; 1994-290911/36.
XX
XX New tri:peptide(s) - inhibit angiotensin I converting enzyme.
XX

```

```

PS Claim 1; Page 2; 4pp; Japanese.
XX
CC This is one of thirteen claimed tripeptides (AAR58569-R58581) which
CC inhibit angiotensin I converting enzyme (with IC50 of 2.9-186.2
XX micromolar). The tripeptides are incorporated into food, e.g. hamburgers
XX
SQ Sequence 3 AA;

Query Match      100.0%; Score 6; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 38
AAR58576
ID AAR58576 standard; peptide; 3 AA.
XX
AC AAR58576;
XX
DT 26-APR-1995 (first entry)
XX
DE Angiotensin I converting enzyme inhibitory tripeptide FRW.
XX
KW angiotensin converting enzyme; inhibitor; food ingredient.
XX
OS Synthetic.
XX
PN JP06220088-A.
XX
PD 09-AUG-1994.
XX
PF 22-JAN-1993; 93JP-00025977.
XX
PR 22-JAN-1993; 93JP-00025977.
XX
PA (ASAH ) ASahi KASEI KOGYO KK.
XX
WPI; 1994-290911/36.
XX
PT New tri:peptide(s) - inhibit angiotensin I converting enzyme.
XX
PS Claim 1; Page 2; 4pp; Japanese.
XX
CC This is one of thirteen claimed tripeptides (AAR58569-R58581) which
CC inhibit angiotensin I converting enzyme (with IC50 of 2.9-186.2
XX micromolar). The tripeptides are incorporated into food, e.g. hamburgers
XX
SQ Sequence 3 AA;

Query Match      100.0%; Score 6; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 40
AAR58570
ID AAR58570 standard; peptide; 3 AA.
XX
AC AAR58570;
XX
DT 26-APR-1995 (first entry)
XX
DE Angiotensin I converting enzyme inhibitory tripeptide LRF.
XX
KW angiotensin converting enzyme; inhibitor; food ingredient.
XX
OS Synthetic.
XX
PN JP06220088-A.
XX
PD 09-AUG-1994.
XX
PF 22-JAN-1993; 93JP-00025977.
XX
PR 22-JAN-1993; 93JP-00025977.
XX
PA (ASAH ) ASahi KASEI KOGYO KK.
XX
WPI; 1994-290911/36.
XX
PT New tri:peptide(s) - inhibit angiotensin I converting enzyme.
XX
PS Claim 1; Page 2; 4pp; Japanese.
XX
CC This is one of thirteen claimed tripeptides (AAR58569-R58581) which
CC inhibit angiotensin I converting enzyme (with IC50 of 2.9-186.2
XX micromolar). The tripeptides are incorporated into food, e.g. hamburgers
XX
SQ Sequence 3 AA;

Query Match      100.0%; Score 6; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 39
AAR58578
ID AAR58578 standard; peptide; 3 AA.
XX
AC AAR58578;
XX
DT 26-APR-1995 (first entry)
XX
DE Angiotensin I converting enzyme inhibitory tripeptide FRV.
XX
KW angiotensin converting enzyme; inhibitor; food ingredient.

```

Qy 1 F 1  
Db 3 F 3

Search completed: February 18, 2006, 07:56:04  
Job time : 99.7895 sec



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 08:01:18 ; Search time 20,8421 Seconds  
(without alignments)  
23.801 Million cell updates/sec

Title: US-09-868-131C-45  
Perfect score: 6  
Sequence: 1 FXXXXX 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:\*

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- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	6	100.0	2	1	US-08-358-160-171 Sequence 171, App
5	6	100.0	2	2	US-09-327-424-2 Sequence 2, Appli
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20	6	100.0	2	2	US-09-419-362-6 Sequence 6, Appli
21	6	100.0	2	2	US-09-419-362-13 Sequence 13, Appl
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24	6	100.0	2	2	US-09-419-362-34 Sequence 34, Appl
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26	6	100.0	2	2	US-09-419-362-40 Sequence 40, Appl
27	6	100.0	2	2	US-09-295-924B-18 Sequence 18, Appl

28	6	100.0	2	2	US-09-551-738B-21 Sequence 21, Appl
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86	6	100.0	3	1	US-08-487-006-210 Sequence 210, App
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91	6	100.0	3	1	US-08-464-456-25 Sequence 25, Appl
92	6	100.0	3	1	US-08-454-950-3 Sequence 3, Appli
93	6	100.0	3	1	US-08-741-678-6 Sequence 6, Appli
94	6	100.0	3	1	US-08-406-192-45 Sequence 45, Appl
95	6	100.0	3	1	US-08-269-929-2 Sequence 2, Appli
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97	6	100.0	3	1	US-08-347-531-1 Sequence 1, Appli
98	6	100.0	3	1	US-08-843-035-24 Sequence 24, Appl
99	6	100.0	3	1	US-08-463-052-25 Sequence 25, Appl
100	6	100.0	3	1	US-08-470-837-11 Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-079-812-140  
; Sequence 140, Application US/08079812  
; Patent No. 5464820  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, James  
; APPLICANT: DONG, Zhengxin  
; TITLE OF INVENTION: SPECIFIC INHIBITORS OF TISSUE KALLIKREIN  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: BAKER & BOTTS, L.L.P.  
; STREET: 555 13th Street, N.W., Suite 500 East  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004-1109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/079,812  
; FILING DATE: 22-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Remenick, James  
; REGISTRATION NUMBER: 36,902  
; REFERENCE/DOCKET NUMBER: 16865-0118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 639-7700  
; TELEFAX: (202) 639-7832  
; INFORMATION FOR SEQ ID NO: 140:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 2  
US-08-079-812-140  
Query Match 100.0%; Score 6; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
DB 2 F 2

RESULT 2  
US-08-079-812-141  
; Sequence 141, Application US/08079812  
; Patent No. 5464820  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, James  
; APPLICANT: DONG, Zhengxin  
; TITLE OF INVENTION: SPECIFIC INHIBITORS OF TISSUE KALLIKREIN  
; NUMBER OF SEQUENCES: 141  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: BAKER & BOTTS, L.L.P.  
; STREET: 555 13th Street, N.W., Suite 500 East  
; CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20004-1109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/079,812  
FILING DATE: 22-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 16865-0118  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 639-7700  
TELEFAX: (202) 639-7832  
INFORMATION FOR SEQ ID NO: 141:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 2  
US-08-079-812-141  
Query Match 100.0%; Score 6; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
DB 2 F 2

RESULT 3  
US-08-127-904-4  
; Sequence 4, Application US/08127904  
; Patent No. 5470951  
; GENERAL INFORMATION:  
; APPLICANT: Eugene Roberts  
; TITLE OF INVENTION: Method For Antagonizing  
; TITLE OF INVENTION: Amnestic Effects of Amyloid n  
; TITLE OF INVENTION: Protein and Improving the  
; TITLE OF INVENTION: Quality of Life in Individuals  
; TITLE OF INVENTION: With Alzheimer Disease  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: City of Hope  
; STREET: 1500 East Duarte Road  
; CITY: Duarte  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91010-0269  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3M Double Density 5 1/4" diskette  
COMPUTER: Wang PC  
OPERATING SYSTEM: MS DOS Version 3.20  
SOFTWARE: Microsoft  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/127,904  
FILING DATE: 29 September 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA: NO. 5470951e  
ATTORNEY/AGENT INFORMATION:  
NAME: Irons, Edward S.  
REGISTRATION NUMBER: 16,541  
REFERENCE/DOCKET NUMBER: No. 5470951e

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
TELEX: NO. 5470951e  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2  
TYPE: Amino Acid  
STRANDEDNESS:  
TOPOLOGY: Unknown  
US-08-127-904-4

Query Match 100.0%; Score 6; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 4  
US-08-358-160-171  
Sequence 171, Application US/08358160  
Patent No. 5663143  
GENERAL INFORMATION:  
APPLICANT: LEY, Arthur C.  
APPLICANT: LADNER, Robert C.  
APPLICANT: GUTERMAN, Sonia K.  
APPLICANT: ROBERTS, Bruce L.  
APPLICANT: MARKLAND, William  
APPLICANT: KENT, Rachel B.  
TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ  
TITLE OF INVENTION: DOMAINS THAT INHIBIT HUMAN NEUTROPHIL ELASTASE  
NUMBER OF SEQUENCES: 234  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W. Suite 300  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,160  
FILING DATE: 16-DEC-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/133,031  
FILING DATE: 13-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/009,319  
FILING DATE: 26-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/664,989  
FILING DATE: 01-MAR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/487,063  
FILING DATE: 02-MAR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/240,160  
FILING DATE: 02-SEP-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Cooper, Iver P.  
REGISTRATION NUMBER: 28,005  
REFERENCE/DOCKET NUMBER: LEY=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528

TELEX: 248633  
INFORMATION FOR SEQ ID NO: 171:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-358-160-171

Query Match 100.0%; Score 6; DB 1; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 5  
US-09-327-424-2  
Sequence 2, Application US/09327424  
Patent No. 6027903  
GENERAL INFORMATION:  
APPLICANT: Eyre, David R  
TITLE OF INVENTION: KIT FOR DETECTING ANALYTE INDICATIVE OF TYPE I COLLAGEN  
TITLE OF INVENTION: RESORPTION IN VIVO (as amended)  
FILE REFERENCE: WROS-1-14019  
CURRENT APPLICATION NUMBER: US/09/327,424  
CURRENT FILING DATE: 1999-06-07  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 2  
TYPE: PRT  
ORGANISM: Human  
FEATURE:  
OTHER INFORMATION: N-telopeptide sequence of type II collagen  
US-09-327-424-2

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 6  
US-08-889-841B-3  
Sequence 3, Application US/08889841B  
GENERAL INFORMATION:  
APPLICANT: Berman, Phillip W.  
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
FILE REFERENCE: 14918-703CIP  
CURRENT APPLICATION NUMBER: US/08/889,841B  
CURRENT FILING DATE: 1997-07-08  
PRIOR APPLICATION NUMBER: US 60/676,737  
PRIOR FILING DATE: 1996-07-08  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 2  
TYPE: PRT  
ORGANISM: HIV  
US-08-889-841B-3

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1



; Sequence 37, Application US/08889841B  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703CIP  
; CURRENT APPLICATION NUMBER: US/08/889,841B  
; CURRENT FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: HIV  
US-08-889-841B-37

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 13  
US-08-889-841B-40  
; Sequence 40, Application US/08889841B  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703CIP  
; CURRENT APPLICATION NUMBER: US/08/889,841B  
; CURRENT FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 40  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: HIV  
US-08-889-841B-40

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 14  
US-09-326-335-2  
; Sequence 2, Application US/09326335  
; Patent No. 6153732  
; GENERAL INFORMATION:  
; APPLICANT: Eyre, David R  
; TITLE OF INVENTION: KIT FOR DETECTING ANALYTE INDICATIVE OF TYPE II  
; TITLE OF INVENTION: COLLAGEN RESORPTION IN VIVO (as amended)  
; FILE REFERENCE: wros-1-14020  
; CURRENT APPLICATION NUMBER: US/09/326,335  
; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Human  
; FEATURE:  
; OTHER INFORMATION: N-telopeptide sequence of type II collagen

US-09-326-335-2

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 15  
US-09-264-709A-29  
; Sequence 29, Application US/09264709A  
; Patent No. 6320024  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Eugene  
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
; FILE REFERENCE: 2124-310  
; CURRENT APPLICATION NUMBER: US/09/264,709A  
; CURRENT FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 08/797,782  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: memory-modulating peptide  
US-09-264-709A-29

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 16  
US-09-264-709A-30  
; Sequence 30, Application US/09264709A  
; Patent No. 6320024  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Eugene  
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and  
; FILE REFERENCE: 2124-310  
; CURRENT APPLICATION NUMBER: US/09/264,709A  
; CURRENT FILING DATE: 1999-03-09  
; PRIOR APPLICATION NUMBER: 08/797,782  
; PRIOR FILING DATE: 1997-02-07  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: memory-modulating peptide  
US-09-264-709A-30

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

```
Db      1 F 1
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-3
Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 20
US-09-419-362-6
; Sequence 6, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-6
Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 21
US-09-419-362-13
; Sequence 13, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13

Db      1 F 1
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223
; CURRENT APPLICATION NUMBER: US/09/295,846B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TMOF or NPF
US-09-295-846B-24
Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 18
US-09-551-737C-24
; Sequence 24, Application US/09551737C
; Patent No. 6586129
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; APPLICANT: Schlessinger, Yaagov
; APPLICANT: Nauwelaers, Sabine M. I.
; TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
; FILE REFERENCE: UF-223C1
; CURRENT APPLICATION NUMBER: US/09/551,737C
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/295,846
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-551-737C-24
Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 19
US-09-419-362-3
; Sequence 3, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
```

```
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-13

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 22
US-09-419-362-17
; Sequence 17, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-17

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 23
US-09-419-362-20
; Sequence 20, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-20

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 24
US-09-419-362-34
; Sequence 34, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-34

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 25
US-09-419-362-37
; Sequence 37, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-37

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 26
US-09-419-362-40
; Sequence 40, Application US/09419362
; Patent No. 6585979
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
```

```
; CURRENT APPLICATION NUMBER: US/09/419,362
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-09-419-362-40
```

```
Query Match 100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 F 1
Db 2 F 2
```

```
RESULT 27
US-09-295-924B-18
; Sequence 18, Application US/09295924B
; Patent No. 6593299
; GENERAL INFORMATION:
; APPLICANT: John, Bennett
; APPLICANT: Alan, Brandt
; APPLICANT: Dov, Borovski
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
; FILE REFERENCE: 4137-120
; CURRENT APPLICATION NUMBER: US/09/295,924B
; CURRENT FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: TMOF analog
US-09-295-924B-18
```

```
Query Match 100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 F 1
Db 2 F 2
```

```
RESULT 28
US-09-551-738B-21
; Sequence 21, Application US/09551738B
; Patent No. 6635265
; GENERAL INFORMATION:
; APPLICANT: Borovsky, Dov
; TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
; FILE REFERENCE: UF-224C1
; CURRENT APPLICATION NUMBER: US/09/551,738B
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/296,113
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TMOF peptide
US-09-551-738B-21
```

```
Query Match 100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 F 1
Db 2 F 2
```

```
RESULT 29
US-09-589-483-16
; Sequence 16, Application US/09589483
; Patent No. 6797488
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS OF PRODUCING ANTI-ANGIOGENIC
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 1440.1031010
; CURRENT APPLICATION NUMBER: US/09/589,483
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/108,536
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: US 60/082,663
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: US 60/067,888
; PRIOR FILING DATE: 1997-12-08
; PRIOR APPLICATION NUMBER: PCT/US98/25892
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Leader peptide on protein produced y prokaryotic
; OTHER INFORMATION: expression system pPICZaa
US-09-589-483-16
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Query Match 100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 F 1
Db 2 F 2
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RESULT 30
US-09-589-483-27
; Sequence 27, Application US/09589483
; Patent No. 6797488
; GENERAL INFORMATION:
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: METHODS OF PRODUCING ANTI-ANGIOGENIC
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: 1440.1031010
; CURRENT APPLICATION NUMBER: US/09/589,483
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: US 60/108,536
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: US 60/082,663
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: US 60/067,888
; PRIOR FILING DATE: 1997-12-08
; PRIOR APPLICATION NUMBER: PCT/US98/25892
; PRIOR FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 34
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Leader peptide on protein produced by eukaryotic
; OTHER INFORMATION: yeast expression system pPIC2a
US-09-589-483-27

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
      |
Db      2 F 2

RESULT 31
US-09-623-548A-211
; Sequence 211, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-211

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
      |
Db      1 F 1

RESULT 32
US-09-623-548A-754
; Sequence 754, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-211

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
      |
Db      1 F 1

RESULT 33
US-09-623-548A-863
; Sequence 863, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 863
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-863

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
      |
Db      2 F 2
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RESULT 34
US-09-623-548A-864
; Sequence 864, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 864
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-864

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 35
US-09-623-548A-1033
; Sequence 1033, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1033
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1033

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 36
US-09-623-548A-1064
; Sequence 1064, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1064
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1064

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 37
US-09-657-276-211
; Sequence 211, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1033

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 36
US-09-623-548A-1064
; Sequence 1064, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1064
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1064

Query Match      100.0%; Score 6; DB 2; Length 2;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 37
US-09-657-276-211
; Sequence 211, Application US/09657276
; Patent No. 6887470
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudreau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110
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; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 211  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-211

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05; 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
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Db 1 F 1

RESULT 38  
US-09-657-276-754  
; Sequence 754, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 754  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-754

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 39  
US-09-657-276-863

; Sequence 863, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 863  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-863

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05; 0; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 40  
US-09-657-276-864  
; Sequence 864, Application US/09657276  
; Patent No. 6887470  
; GENERAL INFORMATION:  
; APPLICANT: Conjuchem, Inc.  
; APPLICANT: Bridon, Dominique  
; APPLICANT: Ezrin, Alan  
; APPLICANT: Milner, Peter  
; APPLICANT: Holmes, Darren  
; APPLICANT: Thibaudau, Karen  
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM  
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD  
; FILE REFERENCE: 2110  
; CURRENT APPLICATION NUMBER: US/09/657,276  
; CURRENT FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/134,406  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 60/153,406  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/159,783  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 1617  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 864  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-657-276-864

US-09-657-276-864

Query Match 100.0%; Score 6; DB 2; Length 2;  
Best Local Similarity 100.0%; Pred. No. 4e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
Db 2 F 2

Search completed: February 18, 2006, 08:02:58  
Job time : 21.8421 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 08:16:49 ; Search time 73.5789 Seconds  
(without alignments)  
34.072 Million cell updates/sec

Title: US-09-868-131C-45

Perfect score: 6

Sequence: 1 FXXXXX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits' satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pgp:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pgp:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pgp:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pgp:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pgp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	6	100.0	2	3	US-09-867-847-34
3	6	100.0	2	3	US-09-867-847-35
4	6	100.0	2	3	US-09-867-847-36
5	6	100.0	2	3	US-09-867-847-37
6	6	100.0	2	3	US-09-867-847-38
7	6	100.0	2	3	US-09-867-847-39
8	6	100.0	2	3	US-09-867-847-40
9	6	100.0	2	3	US-09-867-847-41
10	6	100.0	2	3	US-09-867-847-42
11	6	100.0	2	3	US-09-867-847-43
12	6	100.0	2	3	US-09-867-847-44
13	6	100.0	2	3	US-09-833-245-494
14	6	100.0	2	3	US-09-833-245-1122
15	6	100.0	2	4	US-10-137-867-262
16	6	100.0	2	4	US-10-371-472-3
17	6	100.0	2	4	US-10-371-472-6
18	6	100.0	2	4	US-10-371-472-13
19	6	100.0	2	4	US-10-371-472-17
20	6	100.0	2	4	US-10-371-472-20
21	6	100.0	2	4	US-10-371-472-34
22	6	100.0	2	4	US-10-371-472-37
23	6	100.0	2	4	US-10-371-472-40
24	6	100.0	2	5	US-10-347-145B-118
25	6	100.0	2	5	US-10-347-145B-121
26	6	100.0	2	5	US-10-916-598-15
27	6	100.0	2	5	US-10-825-958-31
28	6	100.0	2	5	US-10-825-958-32
29	6	100.0	2	5	US-10-825-958-33
30	6	100.0	2	5	US-10-825-958-34
31	6	100.0	2	5	US-10-825-958-35
32	6	100.0	2	5	US-10-825-958-36
33	6	100.0	2	5	US-10-825-958-37
34	6	100.0	2	5	US-10-825-958-38
35	6	100.0	2	5	US-10-825-958-39
36	6	100.0	2	5	US-10-825-958-40
37	6	100.0	2	5	US-10-825-958-41
38	6	100.0	2	5	US-10-825-958-42
39	6	100.0	2	5	US-10-975-157-133
40	6	100.0	2	5	US-10-975-157-134
41	6	100.0	2	5	US-10-975-157-144
42	6	100.0	2	5	US-10-975-157-163
43	6	100.0	2	5	US-10-975-157-167
44	6	100.0	2	6	US-11-066-697-211
45	6	100.0	2	6	US-11-066-697-754
46	6	100.0	2	6	US-11-066-697-863
47	6	100.0	2	6	US-11-066-697-864
48	6	100.0	2	6	US-11-066-697-1033
49	6	100.0	2	6	US-11-066-697-1064
50	6	100.0	3	3	US-09-748-061A-14
51	6	100.0	3	3	US-09-824-286-17
52	6	100.0	3	3	US-09-771-192-14
53	6	100.0	3	3	US-09-853-918-7
54	6	100.0	3	3	US-09-850-061A-31
55	6	100.0	3	3	US-09-850-061A-32
56	6	100.0	3	3	US-09-972-475-19
57	6	100.0	3	3	US-09-972-475-20
58	6	100.0	3	3	US-09-895-443-10
59	6	100.0	3	3	US-09-312-762A-11
60	6	100.0	3	3	US-09-312-762A-12
61	6	100.0	3	3	US-09-984-056-25
62	6	100.0	3	3	US-09-982-172-54
63	6	100.0	3	3	US-09-982-172-196
64	6	100.0	3	3	US-09-837-697A-14
65	6	100.0	3	3	US-09-952-432A-6
66	6	100.0	3	3	US-09-952-432A-11
67	6	100.0	3	3	US-09-984-057-25
68	6	100.0	3	3	US-09-900-936-14
69	6	100.0	3	3	US-09-554-000-50
70	6	100.0	3	3	US-09-851-586A-8
71	6	100.0	3	3	US-09-851-586A-50
72	6	100.0	3	3	US-09-851-586A-51
73	6	100.0	3	3	US-09-851-586A-52
74	6	100.0	3	3	US-09-851-586A-53
75	6	100.0	3	3	US-09-772-819-14
76	6	100.0	3	3	US-09-943-944B-25
77	6	100.0	3	3	US-09-943-944B-73
78	6	100.0	3	3	US-09-943-944B-93
79	6	100.0	3	3	US-09-920-306-6
80	6	100.0	3	3	US-09-920-306-36
81	6	100.0	3	3	US-09-920-306-57
82	6	100.0	3	3	US-09-920-306-58
83	6	100.0	3	3	US-09-920-306-64
84	6	100.0	3	3	US-09-920-306-65
85	6	100.0	3	4	US-10-052-817-26
86	6	100.0	3	4	US-10-045-545-12
87	6	100.0	3	4	US-10-121-857-6
88	6	100.0	3	4	US-10-039-876A-3
89	6	100.0	3	4	US-10-039-876A-6
90	6	100.0	3	4	US-10-146-356-14
91	6	100.0	3	4	US-10-255-679-3
92	6	100.0	3	4	US-10-281-652-33
93	6	100.0	3	4	US-10-233-409-38
94	6	100.0	3	4	US-10-163-587A-19
95	6	100.0	3	4	US-10-100-957A-96
96	6	100.0	3	4	US-10-206-699-45
97	6	100.0	3	4	US-10-206-699-46
98	6	100.0	3	4	US-10-206-699-47
99	6	100.0	3	4	US-10-141-531-15
100	6	100.0	3	4	US-10-141-531-17

Sequence 32, Appl  
Sequence 33, Appl  
Sequence 34, Appl  
Sequence 35, Appl  
Sequence 36, Appl  
Sequence 37, Appl  
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Sequence 39, Appl  
Sequence 40, Appl  
Sequence 41, Appl  
Sequence 42, Appl  
Sequence 133, App  
Sequence 134, App  
Sequence 144, App  
Sequence 163, App  
Sequence 167, App  
Sequence 211, App  
Sequence 754, App  
Sequence 863, App  
Sequence 864, App  
Sequence 1033, Ap  
Sequence 1064, Ap  
Sequence 14, Appl  
Sequence 17, Appl  
Sequence 7, Appl  
Sequence 31, Appl  
Sequence 32, Appl  
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Sequence 10, Appl  
Sequence 11, Appl  
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Sequence 25, Appl  
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Sequence 37, Appl  
Sequence 58, Appl  
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Sequence 26, Appl  
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Sequence 3, Appl  
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Sequence 14, Appl  
Sequence 16, Appl  
Sequence 3, Appl  
Sequence 38, Appl  
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Sequence 96, Appl  
Sequence 96, Appl  
Sequence 45, Appl  
Sequence 46, Appl  
Sequence 47, Appl  
Sequence 15, Appl  
Sequence 17, Appl

## ALIGNMENTS

RESULT 1  
US-09-867-847-33  
; Sequence 33, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RES  
; LOCATION: (2)  
; OTHER INFORMATION: CH2CH2SO3H attached at the n-terminus  
US-09-867-847-33

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
DB 1 F 1  
RESULT 2  
US-09-867-847-34  
; Sequence 34, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics

; NAME/KEY: MOD\_RES  
; LOCATION: (2)  
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus  
US-09-867-847-34

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
DB 1 F 1

RESULT 3  
US-09-867-847-35  
; Sequence 35, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; NAME/KEY: MOD\_RES  
; LOCATION: (2)  
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus  
US-09-867-847-35

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
DB 1 F 1

RESULT 4  
US-09-867-847-36  
; Sequence 36, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xiangqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28

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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: CH2CH2SO3H attached at the n-terminus
US-09-867-847-36

Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
Db 1 F 1

RESULT 5
US-09-867-847-37
; Sequence 37, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus
US-09-867-847-37

Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
Db 1 F 1

RESULT 6
US-09-867-847-38
; Sequence 38, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
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; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (2)
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus
US-09-867-847-38
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Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
Db 1 F 1
```

```
RESULT 7
US-09-867-847-39
; Sequence 39, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: HO3SCH2CH2 attached at the c-terminus
US-09-867-847-39
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Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1
Db 1 F 1
```

RESULT 8  
US-09-867-847-40  
; Sequence 40, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: H03SCH2CH2 attached at the c-terminus  
US-09-867-847-40

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1

RESULT 9  
US-09-867-847-41  
; Sequence 41, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: H03SCH2CH2 attached at the c-terminus  
US-09-867-847-41

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1

RESULT 10  
US-09-867-847-42  
; Sequence 42, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: H03SCH2CH2 attached at the c-terminus  
US-09-867-847-42

Query Match 100.0%; Score 6; DB 3; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 1 F 1

RESULT 11  
US-09-867-847-43  
; Sequence 43, Application US/09867847  
; Patent No. US20020094335A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 14445-501 CIP  
; CURRENT APPLICATION NUMBER: US/09/867,847  
; CURRENT FILING DATE: 2001-09-20  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 65  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 2  
; TYPE: PRT



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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: HO3SCH2CH2CH2 attached at the c-terminus
US-09-867-847-43

Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      1 F 1

RESULT 12
US-09-867-847-44
; Sequence 44, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: HO3SCH2CH2CH2 attached at the c-terminus
US-09-867-847-44

Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      1 F 1

RESULT 13
US-09-833-245-494
; Sequence 494, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
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; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-494

Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      1 F 1

RESULT 14
US-09-833-245-1122
; Sequence 1122, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1122
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-1122

Query Match          100.0%; Score 6; DB 3; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 15
US-10-137-867-262
; Sequence 262, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
```

```
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 262
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-262
```

```
Query Match          100.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 F 1
Db      2 F 2
```

```
RESULT 16
US-10-371-472-3
; Sequence 3, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-3
```

```
Query Match          100.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 F 1
Db      2 F 2
```

```
RESULT 17
US-10-371-472-6
; Sequence 6, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-6
```

```
Query Match          100.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 F 1
Db      2 F 2
```

```
RESULT 18
US-10-371-472-13
; Sequence 13, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-13
```

```
Query Match          100.0%; Score 6; DB 4; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 F 1
Db      2 F 2
```

```
RESULT 19
US-10-371-472-17
; Sequence 17, Application US/10371472
; Publication No. US20040052821A1
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703DIV1
; CURRENT APPLICATION NUMBER: US/10/371,472
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US/09/419,362
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: US 08/889,841
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 2
; TYPE: PRT
; ORGANISM: HIV
US-10-371-472-17
```

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 20  
US-10-371-472-20  
; Sequence 20, Application US/10371472  
; Publication No. US20040052821A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/10/371,472  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US/09/419,362  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: HIV  
US-10-371-472-20

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 21  
US-10-371-472-34  
; Sequence 34, Application US/10371472  
; Publication No. US20040052821A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/10/371,472  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US/09/419,362  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 34  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: HIV  
US-10-371-472-34

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 22  
US-10-371-472-37  
; Sequence 37, Application US/10371472  
; Publication No. US20040052821A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/10/371,472  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US/09/419,362  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: HIV  
US-10-371-472-37

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 23  
US-10-371-472-40  
; Sequence 40, Application US/10371472  
; Publication No. US20040052821A1  
; GENERAL INFORMATION:  
; APPLICANT: Berman, Phillip W.  
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE  
; FILE REFERENCE: 14918-703DIV1  
; CURRENT APPLICATION NUMBER: US/10/371,472  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US/09/419,362  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: US 08/889,841  
; PRIOR FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: US 60/676,737  
; PRIOR FILING DATE: 1996-07-08  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 40  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: HIV  
US-10-371-472-40

Query Match 100.0%; Score 6; DB 4; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 24  
US-10-347-145B-118  
; Sequence 118, Application US/10347145B  
; Publication No. US20040248783A1  
; GENERAL INFORMATION:

```
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: KAWABE, TAKUMI
; APPLICANT: KOBAYASHI, HIDETAKA
; TITLE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS HAVING ANTI-PROLIFERATIVE
; TITLE OF INVENTION: ACTIVITY AND/OR THAT AUGMENT NUCLEIC ACID DAMAGING AGENTS OR TR
; FILE REFERENCE: 087533-0301109
; CURRENT APPLICATION NUMBER: US/10/347,145B
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/350,208
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa is Cyclohexyl-alanine
US-10-347-145B-118

Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
Db      1 F 1

RESULT 25
US-10-347-145B-121
; Sequence 121, Application US/10347145B
; Publication No. US20040248783A1
; GENERAL INFORMATION:
; APPLICANT: CanBas Co., Ltd.
; APPLICANT: KAWABE, TAKUMI
; APPLICANT: KOBAYASHI, HIDETAKA
; TITLE OF INVENTION: PEPTIDES AND PEPTIDOMIMETICS HAVING ANTI-PROLIFERATIVE
; TITLE OF INVENTION: ACTIVITY AND/OR THAT AUGMENT NUCLEIC ACID DAMAGING AGENTS OR TR
; FILE REFERENCE: 087533-0301109
; CURRENT APPLICATION NUMBER: US/10/347,145B
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: 60/350,208
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)
; OTHER INFORMATION: Xaa is Cyclohexyl-alanine
US-10-347-145B-121

Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
Db      1 F 1

RESULT 26
US-10-916-598-15
```

```
; Sequence 15, Application US/10916598
; Publication No. US20050042213A1
; GENERAL INFORMATION:
; APPLICANT: Van Gelder, Joel M.
; APPLICANT: Miron, Daphna
; TITLE OF INVENTION: 27413
; FILE REFERENCE: METHODS AND PHARMACEUTICAL COMPOSITIONS FOR MODULATING HEPARANASE
; ACTIVATION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/916,598
; CURRENT FILING DATE: 2004-08-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: N-terminal protecting group - N-carbobenzylxy
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: 7-amino-4-methylcoumarin (AMC) quenched fluorophore linked, amino
; OTHER INFORMATION: acid
US-10-916-598-15

Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 F 1
Db      1 F 1

RESULT 27
US-10-825-958-31
; Sequence 31, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)_
; OTHER INFORMATION: CH2CH2SO3H attached at the n-terminus
US-10-825-958-31

Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
```

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
|  
Db 1 F 1

RESULT 28  
US-10-825-958-32  
; Sequence 32, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (2)-  
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus  
US-10-825-958-32

Query Match 100.0%; Score 6; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
|  
Db 1 F 1

RESULT 29  
US-10-825-958-33  
; Sequence 33, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (2)-  
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus  
US-10-825-958-33

Query Match 100.0%; Score 6; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
|  
Db 1 F 1

RESULT 30  
US-10-825-958-34  
; Sequence 34, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 09/724,842  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 60/168,594  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 2  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides  
; OTHER INFORMATION: or peptidomimetics  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (2)-  
; OTHER INFORMATION: CH2CH2SO3H attached at the n-terminus  
US-10-825-958-34

Query Match 100.0%; Score 6; DB 5; Length 2;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 F 1  
|  
Db 1 F 1

RESULT 31  
US-10-825-958-35  
; Sequence 35, Application US/10825958  
; Publication No. US20050090439A1  
; GENERAL INFORMATION:  
; APPLICANT: Chalfour, Robert  
; APPLICANT: Hebert, Lise  
; APPLICANT: Kong, Xianqi  
; APPLICANT: Gervais, Francine  
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S  
; FILE REFERENCE: 50291/004002  
; CURRENT APPLICATION NUMBER: US/10/825,958

```
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (2)_
; OTHER INFORMATION: CH2CH2CH2SO3H attached at the n-terminus
US-10-825-958-35
```

```
Query Match 100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 F 1
Db 1 F 1
```

```
RESULT 32
US-10-825-958-36
; Sequence 36, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (2)_
; OTHER INFORMATION: CH2CH2CH2CH2SO3H attached at the n-terminus
US-10-825-958-36
```

```
Query Match 100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 F 1
Db 1 F 1
```

```
RESULT 33
US-10-825-958-37
```

```
; Sequence 37, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: HO3SCH2CH2 attached at the c-terminus
US-10-825-958-37
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Query Match 100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 F 1
Db 1 F 1
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RESULT 34
US-10-825-958-38
; Sequence 38, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: HO3SCH2CH2CH2 attached at the c-terminus
US-10-825-958-38
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Query Match      100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
DB      1 F 1

RESULT 35
US-10-825-958-39
; Sequence 39, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2 attached at the c-terminus
US-10-825-958-39

Query Match      100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
DB      1 F 1

RESULT 36
US-10-825-958-40
; Sequence 40, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2CH2 attached at the c-terminus
US-10-825-958-39

Query Match      100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
DB      1 F 1

RESULT 37
US-10-825-958-41
; Sequence 41, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2CH2 attached at the c-terminus
US-10-825-958-41

Query Match      100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
DB      1 F 1

RESULT 38
US-10-825-958-42
; Sequence 42, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2CH2 attached at the c-terminus
US-10-825-958-41
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2 attached at the c-terminus
US-10-825-958-40

Query Match      100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
DB      1 F 1

RESULT 37
US-10-825-958-41
; Sequence 41, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2CH2 attached at the c-terminus
US-10-825-958-41

Query Match      100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
DB      1 F 1

RESULT 38
US-10-825-958-42
; Sequence 42, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: H03SCH2CH2CH2 attached at the c-terminus
US-10-825-958-41
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; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: H03SCH2CH2CH2 attached at the c-terminus
US-10-825-958-42
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```
Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 F 1
      |
Db      1 F 1
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RESULT 39
US-10-975-157-133
; Sequence 133, Application US/10975157
; Publication No. US20050159362A1
; GENERAL INFORMATION:
; APPLICANT: Sircar, Jagadish
; APPLICANT: Alisala, Kashinatham
; APPLICANT: Nikoulin, Igor
; TITLE OF INVENTION: Mediators of Reverse Cholesterol
; TITLE OF INVENTION: Transport for the Treatment of Hypercholesterolemia
; FILE REFERENCE: AVANIR.096CPI
; CURRENT APPLICATION NUMBER: US/10/975,157
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 60/464,667
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: 10/829,855
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically synthesized peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)...(0)
; OTHER INFORMATION: Phe=4,4'-biphenylalanine
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (2)...(0)
US-10-975-157-133
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Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 F 1
      |
Db      1 F 1
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RESULT 40
US-10-975-157-134
; Sequence 134, Application US/10975157
; Publication No. US20050159362A1
; GENERAL INFORMATION:
; APPLICANT: Sircar, Jagadish
; APPLICANT: Alisala, Kashinatham
; APPLICANT: Nikoulin, Igor
; TITLE OF INVENTION: Mediators of Reverse Cholesterol
; TITLE OF INVENTION: Transport for the Treatment of Hypercholesterolemia
; FILE REFERENCE: AVANIR.096CPI
; CURRENT APPLICATION NUMBER: US/10/975,157
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 60/464,667
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: 10/829,855
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 2
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically synthesized peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)...(0)
; OTHER INFORMATION: Phe=4,4'-biphenylalanine
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)...(0)
; OTHER INFORMATION: D-amino acid
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (2)...(0)
US-10-975-157-134
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Query Match          100.0%; Score 6; DB 5; Length 2;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 F 1
      |
Db      1 F 1
```

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Search completed: February 18, 2006, 08:21:12
Job time : 75.5789 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 08:17:29 ; Search time 6.63158 Seconds  
(without alignment)  
12.861 Million cell updates/sec

Title: US-09-868-131C-45  
Perfect score: 6  
Sequence: 1 FXXXXX 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA New:

1: /cgn2\_6/protdata/1/pubpaa/US08\_NEW\_PUB.pep:  
2: /cgn2\_6/protdata/1/pubpaa/US06\_NEW\_PUB.pep:  
3: /cgn2\_6/protdata/1/pubpaa/US07\_NEW\_PUB.pep:  
4: /cgn2\_6/protdata/1/pubpaa/FCR\_NEW\_PUB.pep:  
5: /cgn2\_6/protdata/1/pubpaa/US09\_NEW\_PUB.pep:  
6: /cgn2\_6/protdata/1/pubpaa/US10\_NEW\_PUB.pep:  
7: /cgn2\_6/protdata/1/pubpaa/US11\_NEW\_PUB.pep:  
8: /cgn2\_6/protdata/1/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	3	6	US-10-842-877A-14
2	6	100.0	3	6	US-10-431-638-11
3	6	100.0	3	6	US-10-677-076-10
4	6	100.0	3	7	US-11-056-621-9
5	6	100.0	3	7	US-11-106-623-27
6	6	100.0	3	7	US-11-022-341-27
7	6	100.0	3	7	US-11-022-341-30
8	6	100.0	3	7	US-11-204-187-12
9	6	100.0	3	7	US-11-205-562-12
10	6	100.0	4	6	US-10-503-575-48
11	6	100.0	4	6	US-10-503-575-49
12	6	100.0	4	6	US-10-503-575-59
13	6	100.0	4	6	US-10-503-575-62
14	6	100.0	4	6	US-10-966-648-28
15	6	100.0	4	6	US-10-516-768-38
16	6	100.0	4	6	US-10-997-759-57
17	6	100.0	4	6	US-10-467-657-6678
18	6	100.0	4	6	US-10-467-657-7388
19	6	100.0	4	6	US-10-467-657-8718
20	6	100.0	4	6	US-10-467-657-8745
21	6	100.0	4	6	US-10-467-657-8836
22	6	100.0	4	6	US-10-467-657-8878
23	6	100.0	4	6	US-10-467-657-8908
24	6	100.0	4	6	US-10-467-657-8928
25	6	100.0	4	6	US-10-467-657-8994
26	6	100.0	4	6	US-10-467-657-9125
27	6	100.0	4	6	US-10-467-657-9133
28	6	100.0	4	6	US-10-467-657-9134
29	6	100.0	4	6	US-10-467-657-9196
30	6	100.0	4	6	US-10-914-842A-20
31	6	100.0	4	6	US-10-842-877A-7
32	6	100.0	4	6	US-10-485-788A-66
33	6	100.0	4	6	US-10-485-788A-66
34	6	100.0	4	6	US-10-485-788A-71
35	6	100.0	4	6	US-10-485-788A-96
36	6	100.0	4	6	US-10-485-788A-156
37	6	100.0	4	6	US-10-485-788A-231
38	6	100.0	4	6	US-10-485-788A-276
39	6	100.0	4	6	US-10-485-788A-301
40	6	100.0	4	6	US-10-485-788A-306
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42	6	100.0	4	6	US-10-485-788A-361
43	6	100.0	4	6	US-10-485-788A-441
44	6	100.0	4	6	US-10-485-788A-481
45	6	100.0	4	6	US-10-919-492-5
46	6	100.0	4	6	US-10-919-492-12
47	6	100.0	4	6	US-10-500-878-17
48	6	100.0	4	6	US-10-793-388-1
49	6	100.0	4	6	US-10-793-388-3
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54	6	100.0	4	6	US-10-793-388-8
55	6	100.0	4	6	US-10-793-388-14
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57	6	100.0	4	6	US-10-964-313-35
58	6	100.0	4	6	US-10-964-313-36
59	6	100.0	4	6	US-10-997-081A-1
60	6	100.0	4	6	US-10-997-081A-2
61	6	100.0	4	6	US-10-729-121-58
62	6	100.0	4	6	US-10-431-638-8
63	6	100.0	4	6	US-10-495-464-6
64	6	100.0	4	6	US-10-859-643-701
65	6	100.0	4	6	US-10-859-643-702
66	6	100.0	4	6	US-10-859-643-717
67	6	100.0	4	6	US-10-677-076-8
68	6	100.0	4	6	US-10-677-076-9
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70	6	100.0	4	6	US-10-677-076-12
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73	6	100.0	4	6	US-10-677-076-22
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76	6	100.0	4	6	US-10-895-064-41
77	6	100.0	4	6	US-10-895-064-44
78	6	100.0	4	6	US-10-895-064-122
79	6	100.0	4	6	US-10-895-064-126
80	6	100.0	4	6	US-10-895-064-139
81	6	100.0	4	6	US-10-895-064-141
82	6	100.0	4	6	US-10-895-064-157
83	6	100.0	4	6	US-10-895-064-161
84	6	100.0	4	6	US-10-895-064-165
85	6	100.0	4	6	US-10-895-064-189
86	6	100.0	4	6	US-10-895-064-192
87	6	100.0	4	6	US-10-895-064-205
88	6	100.0	4	6	US-10-895-064-230
89	6	100.0	4	6	US-10-895-064-242
90	6	100.0	4	6	US-10-895-064-257
91	6	100.0	4	6	US-10-895-064-273
92	6	100.0	4	6	US-10-895-064-275
93	6	100.0	4	6	US-10-895-064-298
94	6	100.0	4	6	US-10-895-064-324
95	6	100.0	4	6	US-10-895-064-324
96	6	100.0	4	6	US-10-895-064-324
97	6	100.0	4	6	US-10-895-064-324
98	6	100.0	4	6	US-10-895-064-324

99 6 100.0 4 6 US-10-895-064-329 Sequence 329, App  
100 6 100.0 4 6 US-10-895-064-400 Sequence 400, App

## ALIGNMENTS

RESULT 1  
US-10-842-877A-14  
; Sequence 14, Application US/10842877A  
; Publication No. US20050277595A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dzieroga, Gere  
; TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After  
; FILE REFERENCE: 97-017P7  
; CURRENT APPLICATION NUMBER: US/10/842,877A  
; CURRENT FILING DATE: 2004-05-10  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-842-877A-14

Query Match 100.0%; Score 6; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 2  
US-10-431-638-11  
; Sequence 11, Application US/10431638  
; Publication No. US20060003939A1  
; GENERAL INFORMATION:  
; APPLICANT: The Rockefeller Institute  
; APPLICANT: Steller, Hermann  
; TITLE OF INVENTION: PEPTIDES AND METHODS FOR CELL DEATH REGULATION  
; FILE REFERENCE: P-5004-US  
; CURRENT APPLICATION NUMBER: US/10/431,638  
; CURRENT FILING DATE: 2003-05-08  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-10-431-638-11

Query Match 100.0%; Score 6; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 3  
US-10-677-076-10  
; Sequence 10, Application US/10677076  
; Publication No. US20060014696A1  
; GENERAL INFORMATION:  
; APPLICANT: Findels, M. et al.  
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid

Peptide  
Aggregation Comprising D-Amino Acids  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/677,076  
FILING DATE: 30-Sep-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/920,162  
FILING DATE: 27-AUG-1997  
APPLICATION NUMBER: USSN 08/548,998  
FILING DATE: 27-OCT-1995  
APPLICATION NUMBER: USSN 08/616,081  
FILING DATE: 14-MAR-1996  
APPLICATION NUMBER: USSN 08/703,675  
FILING DATE: 27-AUG-1996  
APPLICATION NUMBER: <Unknown>  
FILING DATE: 21-JUL-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KARA, Catherine J.  
REGISTRATION NUMBER: 41,106  
REFERENCE/DOCKET NUMBER: PPI-016CP4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 1-3  
OTHER INFORMATION: /note= D amino acid  
FEATURE:  
NAME/KEY: Modified site  
LOCATION: 3  
OTHER INFORMATION: /note= phenethylamide C-terminal  
modification  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-677-076-10

Query Match 100.0%; Score 6; DB 6; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04; Indels 0; Gaps 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 4  
US-11-056-621-9  
; Sequence 9, Application US/11056621  
; Publication No. US20050262592A1  
; GENERAL INFORMATION:  
; APPLICANT: Spencer, David  
; APPLICANT: Dickey, Lynn F.  
; APPLICANT: Gasdaska, John R.  
; APPLICANT: Wang, Xiaowei

; APPLICANT: Cox, Kevin M.  
; APPLICANT: Peele, Charles G.  
; TITLE OF INVENTION: EXPRESSION OF PLASMINOGEN AND  
; TITLE OF INVENTION: MICROPLASMINOGEN IN DUCKWEED  
; FILE REFERENCE: 40989/274646  
; CURRENT APPLICATION NUMBER: US/11/056,621  
; CURRENT FILING DATE: 2005-02-11  
; PRIOR APPLICATION NUMBER: US 60/543,487  
; PRIOR FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Substrate for plasmin  
US-11-056-621-9

Query Match 100.0%; Score 6; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 5  
US-11-106-623-27  
; Sequence 27, Application US/11106623  
; Publication No. US20050260733A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: LaVallie, Edward R  
; APPLICANT: Collins-Racie, Lisa A  
; APPLICANT: Corcoran, Christopher J  
; APPLICANT: Agostino, Michael J  
; APPLICANT: Freeman, Bethany A  
; APPLICANT: Arai, Maya  
; APPLICANT: Flannery, Carl R  
; APPLICANT: Jin, Macy X  
; TITLE OF INVENTION: PROTEASES AND USES THEREOF  
; FILE REFERENCE: 031896-034000 (AM101372)  
; CURRENT APPLICATION NUMBER: US/11/106,623  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/562,687  
; PRIOR FILING DATE: 2004-04-16  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 27  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-106-623-27

Query Match 100.0%; Score 6; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 6  
US-11-022-341-27  
; Sequence 27, Application US/11022341  
; Publication No. US20050267016A1  
; GENERAL INFORMATION:  
; APPLICANT: MEDAREX, INC.  
; APPLICANT: Bebbington, Christopher R.  
; APPLICANT: Neider, Matthew H.

; APPLICANT: Cardarelli, Pina M.  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Pan, Chin  
; TITLE OF INVENTION: CD10-Activated Prodrug Compounds  
; FILE REFERENCE: COUL-023/01US  
; CURRENT APPLICATION NUMBER: US/11/022,341  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US/10/167,627  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,596  
; PRIOR FILING DATE: 2001-06-11  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 27  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: chemically synthesized  
US-11-022-341-27

Query Match 100.0%; Score 6; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 7  
US-11-022-341-30  
; Sequence 30, Application US/11022341  
; Publication No. US20050267016A1  
; GENERAL INFORMATION:  
; APPLICANT: MEDAREX, INC.  
; APPLICANT: Bebbington, Christopher R.  
; APPLICANT: Neider, Matthew H.  
; APPLICANT: Cardarelli, Pina M.  
; APPLICANT: Gangwar, Sanjeev  
; APPLICANT: Pickford, Lesley B.  
; APPLICANT: Pan, Chin  
; TITLE OF INVENTION: CD10-Activated Prodrug Compounds  
; FILE REFERENCE: COUL-023/01US  
; CURRENT APPLICATION NUMBER: US/11/022,341  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US/10/167,627  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 60/297,596  
; PRIOR FILING DATE: 2001-06-11  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 30  
; LENGTH: 3  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: chemically synthesized  
US-11-022-341-30

Query Match 100.0%; Score 6; DB 7; Length 3;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 8  
US-11-204-187-12  
; Sequence 12, Application US/11204187



Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0;

Qy	1 F 1
Dd	4 F 4

## RESULT 12

```

US-10-503-575-59
; Sequence 59, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veeelen, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CE
; TITLE OF INVENTION: DETECTING THOSE AND
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-59

```

```
Query Match      : 100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels
```

Qy	1 F 1
Db	4 F 4

RESULT 13

```

US-10-503-575-62
; Sequence 62, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Wouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CE
; TITLE OF INVENTION: DETECTING THOSE AND
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-62

```

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1: Conservative 0; Mismatches 0; Indels

Qy 1 F 1

0; Gaps 0;

D<sub>b</sub> 4 E 4

## RESULT 14

```

US-10-966-648-28
; Sequence 28, Application US/10966648
; Publication No. US20050249734A1
; GENERAL INFORMATION:
; APPLICANT: Sutcliffe, J. Gregor
; APPLICANT: de Lecea, Luis
; APPLICANT: Henriksen, Steven J.
; APPLICANT: Siggins, George R.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
; FILE REFERENCE: 14740A-000640US
; CURRENT APPLICATION NUMBER: US/10/966,648
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 08/648,322
; PRIOR FILING DATE: 1996-05-15
; PRIOR APPLICATION NUMBER: US 08/857,389
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: US 09/766,396
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:shared amino
; OTHER INFORMATION: acids between preprocrystatin and
; OTHER INFORMATION: preprosomatostatin critical for somatostatin
; OTHER INFORMATION: receptor binding
; US-10-966-648-28

```

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels

Qy 1 F 1  
db 1 F 1

RESULT 15

```

RESUL1 13
US-10-516-768-38
; Sequence 38, Application US/10516768
; Publication No. US20050256302A1
; GENERAL INFORMATION:
; APPLICANT: MINAMINO, NAOTO
; APPLICANT: KATAFUCHI, TAKESHI
; TITLE OF INVENTION: NOVEL PEPTIDES HAVING CAMP PRODUCING ACTIVITY
; FILE REFERENCE: 62273(71526)
; CURRENT APPLICATION NUMBER: US/10/516,768
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: PCT/JP03/06641
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: JP 2002-162797
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 38
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Sus sp.
US-10-516-768-38

```

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels

Ov 1 F 1

```
Db          3 F 3

RESULT 16
US-10-997-759-57
; Sequence 57, Application US/10997759
; Publication No. US20050255042A1
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S.
; APPLICANT: Kumaresan, Pappanaicken
; APPLICANT: Denardo, Sally
; APPLICANT: Denardo, Gerald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: On-Demand Cleavable Linkers for Radioconjugates for
; FILE REFERENCE: 02307W-140610US
; CURRENT APPLICATION NUMBER: US/10/997,759
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 60/525,236
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:prototype peptide
; OTHER INFORMATION: linker in radioimmunoconjugate (RIC) in current
; OTHER INFORMATION: clinical use
US-10-997-759-57

Query Match          100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      4 F 4

RESULT 17
US-10-467-657-6678
; Sequence 6678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6678
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6678

Query Match          100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      4 F 4

RESULT 18
US-10-467-657-7388
; Sequence 7388, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7388
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7388

Query Match          100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      3 F 3

RESULT 19
US-10-467-657-8718
; Sequence 8718, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8718
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8718

Query Match          100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      1 F 1

RESULT 20
US-10-467-657-8745
; Sequence 8745, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
```

; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8745  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8745

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 21  
US-10-467-657-8836  
; Sequence 8836, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8836  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8836

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 4 F 4

RESULT 22  
US-10-467-657-8878  
; Sequence 8878, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8878  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8878

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

RESULT 23  
US-10-467-657-8908  
; Sequence 8908, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8908  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Neisseria gonorrhoeae  
US-10-467-657-8908

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 24  
US-10-467-657-8928  
; Sequence 8928, Application US/10467657  
; Publication No. US20050260581A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; APPLICANT: FONTANA Maria Rita  
; APPLICANT: PIZZA Mariagrazia  
; APPLICANT: MASIGNANI Vega  
; APPLICANT: MONACI Elisabetta  
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/467,657  
; CURRENT FILING DATE: 2003-08-11  
; PRIOR APPLICATION NUMBER: GB-0103424.8  
; PRIOR FILING DATE: 2001-02-12  
; NUMBER OF SEQ ID NOS: 9218  
; SOFTWARE: SeqWin99, version 1.04  
; SEQ ID NO 8928

```
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8928

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 25
US-10-467-657-8994
; Sequence 8994, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8994
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8994

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 2 F 2

RESULT 26
US-10-467-657-9125
; Sequence 9125, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9125
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9125

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 2 F 2

RESULT 27
US-10-467-657-9133
; Sequence 9133, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9133
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9133

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 3 F 3

RESULT 28
US-10-467-657-9134
; Sequence 9134, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9134
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9134

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 2 F 2
```



```
RESULT 29
US-10-467-657-9196
; Sequence 9196, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9196
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9196

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      1 F 1

RESULT 30
US-10-914-842A-20
; Sequence 20, Application US/10914842A
; Publication No. US20050260730A1
; GENERAL INFORMATION:
; APPLICANT: FISCHER, PETER MARTIN
; TITLE OF INVENTION: CDK2/CYCLIN A CRYSTALS AND USES THEREOF
; FILE REFERENCE: CCI-032
; CURRENT APPLICATION NUMBER: US/10/914,842A
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: UK 0324465.4
; PRIOR FILING DATE: 2003-10-20
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-914-842A-20

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      4 F 4

RESULT 31
US-10-842-877A-7
; Sequence 7, Application US/10842877A
; Publication No. US2005027595A1
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: diZerega, Gere
; TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After

; TITLE OF INVENTION: Chemotherapy
; FILE REFERENCE: 97-017p7
; CURRENT APPLICATION NUMBER: US/10/842,877A
; CURRENT FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-842-877A-7

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      4 F 4

RESULT 32
US-10-485-788A-46
; Sequence 46, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-46

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      4 F 4

RESULT 33
US-10-485-788A-66
; Sequence 66, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
```

```
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-66

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 4 F 4

RESULT 34
US-10-485-788A-71
; Sequence 71, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-71

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 35
US-10-485-788A-96
; Sequence 96, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US

; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US/10/485,788A
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-96

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 36
US-10-485-788A-156
; Sequence 156, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-156

Query Match      100.0%; Score 6; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 2 F 2

RESULT 37
US-10-485-788A-231
; Sequence 231, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
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; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 231  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: PDZ domain signature sequence  
US-10-485-788A-231

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 4 F 4

RESULT 38  
US-10-485-788A-276  
; Sequence 276, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 276  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-276

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 3 F 3

RESULT 39  
US-10-485-788A-301  
; Sequence 301, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes

; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 301  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-301

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 4 F 4

RESULT 40  
US-10-485-788A-306  
; Sequence 306, Application US/10485788A  
; Publication No. US20050282743A1  
; GENERAL INFORMATION:  
; APPLICANT: Lu, Peter S.  
; APPLICANT: Rabinowitz, Joshua D.  
; APPLICANT: Schweizer, Johannes  
; APPLICANT: Carrick, Deanna Marie  
; APPLICANT: Arbor Vita Corporation  
; TITLE OF INVENTION: Molecular Interactions in Cells  
; FILE REFERENCE: 20054-003320US  
; CURRENT APPLICATION NUMBER: US/10/485,788A  
; CURRENT FILING DATE: 2004-02-03  
; PRIOR APPLICATION NUMBER: US 60/309,841  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/360,061  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 841  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 306  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-788A-306

Query Match 100.0%; Score 6; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6.3e+04;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
Db 4 F 4

Search completed: February 18, 2006, 08:21:39  
Job time : 8.63158 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 07:56:34 ; Search time 14.5263 Seconds  
(without alignments)  
39.742 Million cell updates/sec

Title: US-09-868-131C-45

Perfect score: 6

Sequence: 1 FXXXX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 80:\*

1: Pirl:\*

2: Pirl:\*

3: Pirl:\*

4: Pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	3	3	568328
2	6	100.0	4	1	ECXAA
3	6	100.0	4	2	D41654
4	6	100.0	4	2	S53508
5	6	100.0	4	2	A25844
6	6	100.0	4	2	S39390
7	6	100.0	4	2	JQ1273
8	6	100.0	4	2	A35779
9	6	100.0	4	2	A60418
10	6	100.0	4	2	A32480
11	6	100.0	4	2	ECNK
12	6	100.0	5	2	A32516
13	6	100.0	5	2	A44955
14	6	100.0	5	2	S70615
15	6	100.0	5	2	PS0324
16	6	100.0	5	2	B45525
17	6	100.0	5	2	B61445
18	6	100.0	5	2	A61445
19	6	100.0	5	2	B61168
20	6	100.0	5	2	JH0253
21	6	100.0	5	2	PT0278
22	6	100.0	5	2	A44692
23	6	100.0	5	2	JS0319
24	6	100.0	5	2	PF0644
25	6	100.0	5	4	A58728
26	6	100.0	6	2	A61096
27	6	100.0	6	2	A60986
28	6	100.0	6	2	S11024
29	6	100.0	6	2	I51317

30	6	100.0	6	2	I37263	Y protein - human
31	6	100.0	6	2	B35640	cerbellar degener
32	6	100.0	6	2	I59142	platelet-derived g
33	6	100.0	6	2	A41946	T-cell receptor ga
34	6	100.0	6	2	PD0028	pev-kinin 2 - pena
35	6	100.0	6	2	A27696	contraction-inhibi
36	6	100.0	6	2	B27696	locustakinin - mig
37	6	100.0	6	2	A61068	neuropeptide GNFR
38	6	100.0	6	2	A43129	hypothalamic hepta
39	6	100.0	7	1	NYR7	dermorphin - Ronde
40	6	100.0	7	1	A61324	Met-enkephalin-Arg
41	6	100.0	7	2	A60224	dermorphin (Lys-7)
42	6	100.0	7	2	S36662	dermorphin (Trp-4,
43	6	100.0	7	2	S21230	Ig heavy chain V r
44	6	100.0	7	2	PH1408	phosphotransferase
45	6	100.0	7	2	B3127	hypothetical prote
46	6	100.0	7	2	I40504	180K exoantigen -
47	6	100.0	7	2	H33098	hucolin, 75K chain
48	6	100.0	7	2	S68004	Ig mu chain D regi
49	6	100.0	7	2	E33932	pev-kinin 1 - pena
50	6	100.0	7	2	PT0665	T-cell receptor be
51	6	100.0	7	2	PD0029	pullulanase (EC 3.
52	6	100.0	7	2	PN0649	protein kinase C 1
53	6	100.0	7	2	A59489	RNA-directed DNA p
54	6	100.0	7	2	B35890	sex pheromone cCP1
55	6	100.0	7	2	A25269	glucose isomerase
56	6	100.0	7	2	A30812	FMRFamide-related
57	6	100.0	7	2	S17976	callifmrfamide 11
58	6	100.0	7	2	PC2132	tubulin beta-3 cha
59	6	100.0	7	2	B44787	hypothetical prote
60	6	100.0	7	2	S33567	peptidyl-di-peptida
61	6	100.0	7	2	S08606	adipokinetic hormo
62	6	100.0	8	2	A35223	adipokinetic hormo
63	6	100.0	8	2	A33995	adipokinetic hormo
64	6	100.0	8	2	A44960	red pigment-concen
65	6	100.0	8	2	B44960	adipokinetic hormo
66	6	100.0	8	2	A58620	hypertrahalosemic
67	6	100.0	8	2	S11545	hypertrahalosemic
68	6	100.0	8	2	S55310	cholecystokinin -
69	6	100.0	8	2	A61348	cholecystokinin -
70	6	100.0	8	2	S10596	Ig heavy chain V r
71	6	100.0	8	2	S08995	capsid protein VP-
72	6	100.0	8	2	S08996	protein Q300040 -
73	6	100.0	8	2	A49823	polygalacturonase
74	6	100.0	8	2	B49823	158K exoantigen -
75	6	100.0	8	2	A28004	P element, P cytot
76	6	100.0	8	2	A43976	serum albumin - do
77	6	100.0	8	2	B43976	fibroblast growth
78	6	100.0	8	2	PQ0012	T-cell receptor al
79	6	100.0	8	2	A43001	T-cell receptor ga
80	6	100.0	8	2	PH1407	telomeric and tetr
81	6	100.0	8	2	FL0184	Na+-transporting A
82	6	100.0	8	2	PA0032	tpsa protein - Erw
83	6	100.0	8	2	S13661	cellulase (EC 3.2.
84	6	100.0	8	2	B33099	R-phycocerythrin ga
85	6	100.0	8	2	A39892	glucose-6-phosphat
86	6	100.0	8	2	B45800	inulinase (EC 3.2.
87	6	100.0	8	2	A42057	spasmogenic toxin
88	6	100.0	8	2	PH0803	neuropeptide M-1 -
89	6	100.0	8	2	PC4372	leucokinin V - Mad
90	6	100.0	8	2	S66296	leucokinin VI - Ma
91	6	100.0	8	2	S37141	
92	6	100.0	8	2	S21273	
93	6	100.0	8	2	A37521	
94	6	100.0	8	2	S11078	
95	6	100.0	8	2	PT0030	
96	6	100.0	8	2	A46306	
97	6	100.0	8	2	A05169	
98	6	100.0	8	2	JS0315	
99	6	100.0	8	2	JS0316	
100	6	100.0	8	2		

## ALIGNMENTS

RESULT 1  
 S68328  
 blood cell protein A - Molgula manhattensis (fragment)  
 C:Species: Molgula manhattensis  
 C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
 C:Accession: S68328  
 R:Taylor, S.W.; Ross, M.M.; Waite, J.H.  
 Arch. Biochem. Biophys. 324, 228-240, 1995  
 A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from the blood of the sea anemone *Molgula manhattensis*  
 A:Reference number: S68325; MUID:96132650; PMID:8554314  
 A:Accession: S68328  
 A:Molecule type: protein  
 A:Residues: 1-3 <TAY>  
 A:Cross-references: UNIPARC:UPI000017CEA2

Query Match 100.0%; Score 6; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 2 F 2

RESULT 2  
 ECXAA  
 antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)  
 C:Species: Anthopleura elegantissima  
 C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
 C:Accession: A26666  
 R:Grimmelikhuijzen, C.J.P.; Graff, D.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986  
 A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemone *Anthopleura elegantissima*  
 A:Reference number: A26666; MUID:87092339; PMID:2879288  
 A:Accession: A26666  
 A:Molecule type: protein  
 A:Residues: 1-4 <GRI>  
 A:Cross-references: UNIPROT:PI0419; UNIPARC:UPI00001733AF  
 C:Comment: The function of this peptide is not known but it could act as a transmitter and modulate the function of the neurotransmitter serotonin.  
 C:Superfamily: RFamide neuropeptide  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 100.0%; Score 6; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 4 F 4

RESULT 3  
 D41654  
 hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)  
 C:Species: Haemophilus parainfluenzae  
 C>Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 24-Feb-1995  
 C:Accession: D41654  
 R:Kroll, J.S.; Langford, P.R.; Loynds, B.M.  
 J. Bacteriol. 173, 7445-7457, 1991  
 A:Title: Copper-zinc superoxide dismutase of *Haemophilus influenzae* and *Haemophilus parainfluenzae*  
 A:Reference number: A41654; MUID:92041655; PMID:1938942  
 A:Accession: D41654  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-4 <KOE>  
 A:Cross-references: UNIPARC:UPI000017AB26

Query Match 100.0%; Score 6; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 3 F 3

RESULT 4  
 S53508  
 starvation-induced ribonuclease - tomato  
 C:Species: Lycopersicon esculentum (tomato)  
 C>Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 C:Accession: S53508  
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
 Plant Mol. Biol. 27, 477-485, 1995  
 A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases from *Lycopersicon esculentum*  
 A:Reference number: S53506; MUID:95201242; PMID:7894013  
 A:Accession: S53508  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <KOE>  
 A:Cross-references: UNIPARC:UPI000017B092

Query Match 100.0%; Score 6; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 1 F 1

RESULT 5  
 A25844  
 antho-RF amide neuropeptide - sea pansy (Renilla koellikeri)  
 C:Species: Renilla koellikeri (Koelliker's sea pansy)  
 C>Date: 21-May-1988 #sequence\_revision 30-Sep-1993 #text\_change 11-Jul-1997  
 C:Accession: A25844  
 R:Grimmelikhuijzen, C.J.P.; Groeger, A.  
 FEBS Lett. 211, 105-108, 1987  
 A:Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid *Renilla koellikeri*  
 A:Reference number: A25844  
 A:Accession: A25844  
 A:Molecule type: protein  
 A:Residues: 1-4 <GRI>  
 A:Cross-references: UNIPARC:UPI00001733AF  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 4 F 4

RESULT 6  
 S39390  
 myosin-light-chain kinase (EC 2.7.1.117), smooth muscle - turkey (fragment)  
 C:Species: Meleagris gallopavo (common turkey)  
 C>Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 07-May-1999  
 C:Accession: S39390  
 R:Komatsu, H.; Ikebe, M.  
 Biochem. J. 296, 53-58, 1993  
 A:Title: Affinity labelling of smooth-muscle myosin light-chain kinase with 5'-[p-(fluoromethyl)-3-thio]adenosine triphosphate  
 A:Reference number: S39390; MUID:94071841; PMID:8250857  
 A:Accession: S39390  
 A:Molecule type: protein

A;Residues: 1-4 <KOW>  
 A;Cross-references: UNIPARC:UPI000017C048  
 A;Experimental source: Gizzard  
 C;Keywords: phosphotransferase; smooth muscle

Query Match 100.0%; Score 6; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Gaps 0;

QY 1 F 1  
 |  
 Db 4 F 4

## RESULT 7

JQ1273

neuropeptide Antho-Kaamide - sea anemone (Anthopleura elegantissima)

C;Species: Anthopleura elegantissima

C;Date: 31-Mar-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004

C;Accession: JQ1273

R;Nothacker, H.P.; Rinehart, K.L.; Grimmelikhuijzen, C.J.P.

Biochem. Biophys. Res. Commun. 179, 1205-1211, 1991

A;Title: Isolation of L-3-phenyllactyl-L-Phe-Lys-Ala-NH<sub>2</sub> (Antho-Kaamide), a novel neuropeptide from Anthopleura elegantissima

A;Reference number: JQ1273; MUID:92028852; PMID:1681803

A;Accession: JQ1273

A;Molecule type: protein

A;Residues: 1-4 <NOP>

A;Cross-references: UNIPROT:P58705; UNIPARC:UPI000012A703

C;Comment: The carboxyl-terminal amide probably arises from cleavage of a following glycosylated peptide: amideated carboxyl end; neuropeptide; phenyllactylation

C;Keywords: amideated carboxyl end; neuropeptide; phenyllactylation

F;1/Modified site: L-3-phenyllactic acid (Phe) #status experimental

F;4/Modified site: amideated carboxyl end (Ala) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 1 F 1

## RESULT 8

A35779

neuropeptide Antho-RNamide - sea anemone (Anthopleura elegantissima)

C;Species: Anthopleura elegantissima

C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 09-Jul-2004

C;Accession: A35779

R;Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Nothacker, Natl. Acad. Sci. U.S.A. 87, 5410-5414, 1990

A;Title: Isolation of L-3-phenyllactyl-L-Leu-Arg-Asn-NH<sub>2</sub> (Antho-RNamide), a sea anemone neuropeptide

A;Reference number: A35779; MUID:90319122; PMID:1973541

A;Accession: A35779

A;Molecule type: protein

A;Residues: 1-4 <GRI>

A;Cross-references: UNIPROT:P58707; UNIPARC:UPI000012A36

C;Comment: The L-3-phenyllactyl blocking group probably arises from an amino-terminal phenyllactylation

C;Keywords: amideated carboxyl end; neuropeptide; phenyllactylation

F;1/Modified site: L-3-phenyllactic acid (Phe) #status experimental

F;4/Modified site: amideated carboxyl end (Asn) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 1 F 1

## RESULT 9

A60418

FMRamide - polychaete (Nereis virens)

C;Species: Nereis virens (sandworm)

C;Date: 11-Feb-1993 #sequence\_revision 11-Feb-1993 #text\_change 09-Jul-2004

C;Accession: A60418

R;Krajniak, K.G.; Price, D.A.

Peptides 11, 75-77, 1990

A;Title: Authentic FMRamide is present in the polychaete Nereis virens.

A;Reference number: A60418; MUID:90259866; PMID:2342992

A;Accession: A60418

A;Molecule type: protein

A;Residues: 1-4 <KRA>

A;Cross-references: UNIPROT:P01162; UNIPARC:UPI000012AADS

C;Keywords: amideated carboxyl end; neuropeptide

F;4/Modified site: amideated carboxyl end (Phe) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 1 F 1

## RESULT 10

A32480

achatin-I - giant African snail

N;Contains: achatin-II

C;Species: Achatina fulica (giant African snail)

C;Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 09-Jul-2004

C;Accession: A32480

R;Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Iwashita, T.; Watanabe, K.; Funase, K.; Su

Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989

A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica

A;Reference number: A32480; MUID:89273551; PMID:2597281

A;Accession: A32480

A;Molecule type: protein

A;Residues: 1-4 <KAM>

A;Cross-references: UNIPROT:P35904; UNIPARC:UPI0000125223

A;Note: stereochemistry of the active form confirmed by chemical synthesis

R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto

FEBS Lett. 307, 253-256, 1992

A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro

(H-Gly-Phe-Ala-Asp-OH).

A;Reference number: A44691; MUID:92354723; PMID:1644179

A;Contents: annotation; X-ray crystallography, 0.85 angstroms

A;Note: achatin-II has L-phenylalanine

C;Keywords: D-amino acid

F;2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 2 F 2

## RESULT 11

ECNK

cardioexcitatory neuropeptide FMRamide - sunray clam

C;Species: Macrocallista nimbosa (sunray clam)

C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004

C;Accession: A01426

R;Price, D.A.; Greenberg, M.J.

Science 197, 670-671, 1977

A;Title: Structure of a molluscan cardioexcitatory neuropeptide.

A;Reference number: A01426; MUID:77215956; PMID:877582

A;Accession: A01426

A;Molecule type: protein

A;Residues: 1-4 <PRI>

A;Cross-references: UNIPROT:P01162; UNIPARC:UPI000012AADS

A;Note: the active peptide was also synthesized

C;Comment: This peptide was purified from pooled extracts of cerebral, pedal, and visceral action in molluscs; its exact physiological role is not yet established.

C;Keywords: amidated carboxyl end; neuropeptide  
F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

## RESULT 12

A32516  
cholecystokinin-5 - dog  
N;Alternate names: CCK-5  
C;Species: Canis lupus familiaris (dog)  
C;Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 18-Aug-2000  
C;Accession: A32516  
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.  
Am. J. Physiol. 252, G272-G275, 1987  
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intestine  
A;Reference number: A32516; MUID:87153871; PMID:3826354  
A;Accession: A32516  
A;Molecule type: protein  
A;Residues: 1-5 <SHI>  
A;Cross-references: UNIPARC:UPI0000147D25  
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecystokinin  
C;Superfamily: gastrin  
C;Keywords: amidated carboxyl end; neuropeptide  
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 5 F 5

## RESULT 13

A44955  
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)  
C;Species: Vibrio harveyi  
C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 26-May-2000  
C;Accession: A44955  
R;Paquette, O.; Tu, S.C.  
Photochem. Photobiol. 50, 817-825, 1989  
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib  
A;Reference number: A44955; MUID:90175700; PMID:2626493  
A;Accession: A44955  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5 <PAQ>  
A;Cross-references: UNIPARC:UPI000017AAD8  
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

## RESULT 14

S70615  
endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)  
N;Alternate names: xylanase

C;Species: Streptomyces sp.  
A;Variety: Chainia sp. NCL 82.5.1  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
C;Accession: S70615  
R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.  
Biochem. J. 316, 771-775, 1996  
A;Title: Structural environment of an essential cysteine residue of xylanase from Chain:  
A;Reference number: S70615; MUID:96265041; PMID:8670151  
A;Accession: S70615  
A;Molecule type: protein  
A;Residues: 1-5 <RAO>  
A;Cross-references: UNIPARC:UPI000017AE36  
A;Experimental source: Chainia sp. strain NCL 82.5.1  
A;Note: the source is designated as Chainia sp.  
C;Function:  
A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans  
A;Pathway: fermentation of hemicellulose into ethanol  
C;Keywords: glycosidase; hydrolase

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

## RESULT 15

PS0324  
ribulose-bisphosphate carboxylase activase III - rice (strain Nihonbare) (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 02-Jul-1998  
C;Accession: PS0324  
R;Tsugita, A.  
submitted to JIPID, April 1993  
A;Reference number: PS0206  
A;Accession: PS0324  
A;Molecule type: protein  
A;Residues: 1-5 <TSU>  
A;Cross-references: UNIPARC:UPI000017B11D  
A;Experimental source: leaf, chlorophyll

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

## RESULT 16

B45525  
actin I - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C;Accession: B45525  
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak  
Mol. Biochem. Parasitol. 35, 167-176, 1989  
A;Title: Stage-specific expression and genomic organization of the actin genes of the ma  
A;Reference number: A45525; MUID:89364996; PMID:2671721  
A;Accession: B45525  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <WES>  
A;Cross-references: UNIPARC:UPI000017B5EC; GB:J03988  
A;Note: the authors translated the codon GAA for residue 3 as Gly  
C;Comment: The actin I gene contains no introns.

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 F 1  
|  
Db 5 F 5

## RESULT 17

B61445  
Leu-enkephalin - blue mussel  
C;Species: Mytilus edulis (blue mussel)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
C;Accession: B61445  
R;Leung, M.K.; Stefano, G.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
A;Reference number: A61445; MUID:84144823; PMID:6583690  
C;Accession: B61445  
A;Molecule type: protein  
A;Residues: 1-5 <LEU>  
A;Cross-references: UNIPARC:UPI000002D557  
A;Experimental source: pedal ganglia  
C;Keywords: neuropeptide; opioid peptide

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 4 F 4

## RESULT 18

A61445  
Met-enkephalin - blue mussel  
C;Species: Mytilus edulis (blue mussel)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
C;Accession: A61445  
R;Leung, M.K.; Stefano, G.B.  
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
A;Reference number: A61445; MUID:84144823; PMID:6583690  
C;Accession: A61445  
A;Molecule type: protein  
A;Residues: 1-5 <LEU>  
A;Cross-references: UNIPARC:UPI000002CF9B  
A;Experimental source: pedal ganglia  
C;Keywords: neuropeptide; opioid peptide

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 4 F 4

## RESULT 19

B61168  
cocoanase (EC 3.4.21.-) - Chinese oak silkworm (fragment)  
C;Species: Antheraea pernyi (Chinese oak silkworm)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: B61168  
R;Kramer, K.J.; Felsted, R.L.; Law, J.H.  
J. Biol. Chem. 248, 3021-3028, 1973  
A;Title: Cocoanase. V. Structural studies on an insect serine protease.  
A;Reference number: A61168; MUID:73165540; PMID:4735570  
C;Accession: B61168  
A;Molecule type: protein  
A;Residues: 1-5 <KRA>  
A;Cross-references: UNIPARC:UPI000017BE47  
C;Keywords: hydrolase; serine proteinase; zymogen

F;1-5/Product: cocoanase (fragment) #status experimental <MAT>

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 5 F 5

## RESULT 20

JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
C;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Cross-references: UNIPARC:UPI000017BF42  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric, and of the circular muscle of the gastro-intestinal junction.

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

## RESULT 21

PT0278  
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0278  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
C;Accession: PT0278  
A;Molecule type: DNA  
A;Residues: 1-5 <YAM>  
A;Cross-references: UNIPARC:UPI000017C202  
A;Experimental source: B lymphocyte  
C;Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

## RESULT 22

A44692  
fulicin - giant African snail  
C;Species: Achatina fulica (giant African snail)  
C;Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: A44692  
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.;  
Biochem. Biophys. Res. Commun. 178, 486-493, 1991  
A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from

A:Reference number: A44692; MUID:91315471; PMID:1859408

A:Accession: A44692

A:Molecule type: protein

A:Residues: 1-5 <OHT>

A:CROSS-references: UNIPROT:P35905; UNIPARC:UPI00001567CA

C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide

F:2/Modified site: D-asparagine (Asn) #status experimental

F:5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

#### RESULT 23

JS0319

subesophageal ganglion pentapeptide - house cricket

C:Species: Acheta domesticus (house cricket)

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

A:Accession: JS0319

R:Wicker, C.; Wicker, C.

Comp. Biochem. Physiol. C 88, 185-187, 1987

A:Title: Isolation and structure of a peptide isolated from the subesophageal ganglion

A:Reference number: JS0319

A:Accession: JS0319

A:Molecule type: protein

A:Residues: 1-5 <WIC>

A:CROSS-references: UNIPROT:P19991; UNIPARC:UPI00001361CE

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 5 F 5

#### RESULT 24

PT0644

T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

A:Accession: PT0644

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0644

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-5 <FEE>

A:CROSS-references: UNIPROT:Q92276; UNIPARC:UPI000017C7D2

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 100.0%; Score 6; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 4 F 4

#### RESULT 25

AS5728

Serratia marcescens

C:Species: Serratia marcescens

C:Date: 10-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 12-Feb-1998  
C:Accession: AS8728

R:Matsumura, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.

J. Bacteriol. 174, 1769-1776, 1992

A:Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent an

A:Reference number: AS8728; MUID:92193360; PMID:1548227

A:Accession: AS8728

A>Status: unencoded polypeptide

A:Molecule type: protein

A:Residues: 1-5 <MAT>

A:CROSS-references: UNIPARC:UPI0000017CF12

A:Experimental source: strain NS 25

C:Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation

C:Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded

F:1/Modified site: D-leucine (Leu) #status experimental

F:4/Modified site: D-phenylalanine (Phe) #status experimental

F:1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status exper

Query Match 100.0%; Score 6; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 4 F 4

#### RESULT 26

A61049

halo-toxin - Pseudomonas syringae pv. mori

C:Species: Pseudomonas syringae pv. mori

A:Note: host mulberry tree

C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997

A:Accession: A61049

R:Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.

Chem. Lett. 00, 679-680, 1989

A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri

A:Reference number: A61049

A:Accession: A61049

A:Molecule type: protein

A:Residues: 1-6 <KAJ>

A:CROSS-references: UNIPARC:UPI00000352A6

A:Note: sequence confirmed by synthesis

C:Comment: This toxin is one of the etiological agents of halo bright disease in mulberry

C:Keywords: toxin

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 2 F 2

#### RESULT 27

A60986

N-formyl oligopeptide - Escherichia coli (fragment)

C:Species: Escherichia coli

C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993

A:Accession: A60986

R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.

Experientia 45, 1097-1099, 1989

A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionyl

A:Reference number: A60986; MUID:90092408; PMID:2689204

A:Accession: A60986

A:Molecule type: protein

A:Residues: 1-6 <ERO>

A:CROSS-references: UNIPARC:UPI0000017AA56

C:Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.

F:1/Modified site: N-formylmethionine #status experimental

Query Match 100.0%; Score 6; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 28  
S11024  
hydrogenulfite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)  
N:Alternate names: bisulfite reductase; desulfofuscinidin  
C:Species: Desulfovibrio thermophilus  
C:Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C:Accession: S11024  
R:Fauque, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; I  
Biochim. Biophys. Acta 1040, 112-118, 1990  
A:Title: Purification and characterization of bisulfite reductase (desulfofuscinidin) from  
A:Reference number: S11024; MUID:90335276; PMID:2165817  
A:Accession: S11024  
A:Molecule type: protein  
A:Residues: 1-6 <FAU>  
A:Cross-references: UNIPARC:UPI000017AB74  
C:Keywords: oxidoreductase

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 5 F 5

RESULT 29  
I51317  
bHLH transcription factor inhibitor - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I51317  
R:Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.  
Mech. Dev. 50, 119-130, 1995  
A:Title: Id gene activity during Xenopus embryogenesis.  
A:Reference number: I51316; MUID:95344988; PMID:7619724  
A:Accession: I51317  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <ZHA>  
A:Cross-references: UNIPARC:UPI000011EA87; GB:S79038; NID:G1042006; PIDN:AAD14294.1; PID  
C:Genetics:  
A:Gene: Xid1b

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 6 F 6

RESULT 30  
I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waechter, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna  
A:Reference number: I37263; MUID:93010691; PMID:1396344  
A:Accession: I37263  
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: UNIPARC:UPI000011EBEF; EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID  
C:Genetics:  
A:Gene: CREB

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 31  
B35640  
cerebellar degeneration-related protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 24-Jun-1993  
C:Accession: B35640  
R:Chen, Y.T.; Rettig, W.J.; Venamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990  
A:Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal ma  
A:Reference number: A35640; MUID:90222173; PMID:2326268  
A:Accession: B35640  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-6 <CHE>  
A:Cross-references: UNIPARC:UPI000017C63A

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

RESULT 32  
I59142  
platelet-derived growth factor B chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I59142  
R:Pech, M.; Gazit, A.; Arnstein, P.; Aaronson, S.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989  
A:Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the normal  
A:Reference number: I59142; MUID:89202393; PMID:2649890  
A:Accession: I59142  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <RES>  
A:Cross-references: UNIPARC:UPI000011E8C4; GB:M26180; NID:G516624; PIDN:AAA39905.1; PID

Query Match 100.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

RESULT 33  
A41946  
T-cell receptor gamma chain (1t.22) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: A41946  
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A:Reference number: A41946; MUID:92049316; PMID:1658619

C:Accession: A41946

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <WHE>

A:Cross-references: UNIPARC:UPI000017C865

C:Keywords: T-cell receptor

Query Match 100.0%; Score 6; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

|

6 F 6

RESULT 34

PD0028

pev-kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment)

C:Species: Penaeus vannamei

C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 19-May-2000

C:Accession: PD0028

R:Nieto, J.; Velaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devreese,

Biochem. Biophys. Res. Commun. 248, 406-411, 1998

A:Title: Identification of one tachykinin- and two kinin-related peptides in the brain of

A:Reference number: PD0027; MUID:98342103; PMID:9675150

A:Accession: PD0028

A:Molecule type: protein

A:Residues: 1-6 <NIE>

A:Cross-references: UNIPARC:UPI000017C80B

C:Comment: This peptide belongs to myotropic neuropeptides.

Query Match 100.0%; Score 6; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

|

2 F 2

RESULT 35

A27696

contraction-inhibiting peptide I - blue mussel

C:Species: Mytilus edulis (blue mussel)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C:Accession: A27696

R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988

A:Title: Structures and actions of Mytilus inhibitory peptides.

A:Reference number: A90142; MUID:88240357; PMID:3377776

A:Accession: A27696

A:Molecule type: protein

A:Residues: 1-6 <HIR>

A:Cross-references: UNIPROT:P13736; UNIPARC:UPI0000127951

C:Keywords: amidated carboxyl end

F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

|

5 F 5

RESULT 36

B27696

contraction-inhibiting peptide II - blue mussel

C:Species: Mytilus edulis (blue mussel)

C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C:Accession: B27696

R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.

Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988

A:Title: Structures and actions of Mytilus inhibitory peptides.

A:Reference number: A90142; MUID:88240357; PMID:3377776

A:Accession: B27696

A:Molecule type: protein

A:Residues: 1-6 <HIR>

A:Cross-references: UNIPROT:P13737; UNIPARC:UPI0000127952

C:Keywords: amidated carboxyl end

F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 100.0%; Score 6; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1

|

5 F 5

## RESULT 39

NYPG7  
hypothalamic heptapeptide - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 01-Sep-1981 #sequence\_revision 01-Sep-1981 #text\_change 09-Jul-2004  
C:Accession: A01417  
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, H.M. Metab. Res. 13, 228-232, 1981  
A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-release  
A;Reference number: A01417; MUID:81213980; PMID:6263778  
A;Accession: A01417  
A:Molecule type: protein  
A;Residues: 1-7 <CHA>  
A;Cross-references: UNIPROT:P01153; UNIPARC:UPI000012CF06  
C;Superfamily: hypothalamic heptapeptide  
C;Keywords: hypothalamus

Query Match 100.0%; Score 6; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 1 F 1

## RESULT 40

A61324  
dermorphin - Rohde's leaf frog  
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C:Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: A61324  
R;Montecucchi, P.C.; De Castiglione, R.; Erspaner, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz  
A;Reference number: A61324; MUID:82029915; PMID:7287302  
A;Accession: A61324  
A:Molecule type: protein  
A;Residues: 1-7 <MON>  
A;Cross-references: UNIPARC:UPI00002DEA5  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
C;Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin  
F;2/Modified site: D-alanine (Ala) #status experimental  
F;6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F;7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 100.0%; Score 6; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
|  
Db 3 F 3

Search completed: February 18, 2006, 08:01:48  
Job time : 17.5263 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 07:51:13 ; Search time 90.9474 Seconds  
(without alignments)  
46.545 Million cell updates/sec

Title: US-09-868-131C-45

Perfect score: 6

Sequence: 1 FXXXXX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	100.0	4	1	ACH1_ACHFU
2	6	100.0	4	1	FAR3_HIRME
3	6	100.0	4	1	FAR4_HIRME
4	6	100.0	4	1	FFKA_ANTEL
5	6	100.0	4	1	FLRF_HELTI
6	6	100.0	4	1	FLRF_HIRME
7	6	100.0	4	1	FLRN_ANTEL
8	6	100.0	4	1	FMRF_HELTI
9	6	100.0	4	1	FMRF_HIRME
10	6	100.0	4	1	FMRF_MACNI
11	6	100.0	4	1	FMRF_NERVI
12	6	100.0	4	1	FMRF_ANTEL
13	6	100.0	4	1	OCPI_OCTMI
14	6	100.0	4	2	Q16047_HUMAN
15	6	100.0	5	1	ALL14_CARMA
16	6	100.0	5	1	E103_LITRU
17	6	100.0	5	1	E104_LITRU
18	6	100.0	5	1	FARP_ARTTR
19	6	100.0	5	1	FARP_CHICK
20	6	100.0	5	1	PAP2_PARMA
21	6	100.0	5	1	RBE11_LITRU
22	6	100.0	5	1	RBE21_LITRU
23	6	100.0	5	1	RBE31_LITRU
24	6	100.0	5	1	RBE32_LITRU
25	6	100.0	5	1	SUGA_ACHDO
26	6	100.0	5	1	TPIS_CANFA
27	6	100.0	5	1	UC22_MAIZE
28	6	100.0	6	1	CIP1_MYTED
29	6	100.0	6	1	CIP2_MYTED
30	6	100.0	6	1	E101_LITRU
31	6	100.0	6	1	FARP_MONEX

32	6	100.0	6	1	LOK1_LOCMI
33	6	100.0	6	1	PYF1_PENMO
34	6	100.0	7	1	ALL2_CARMA
35	6	100.0	7	1	ALL3_CARMA
36	6	100.0	7	1	ALL4_CARMA
37	6	100.0	7	1	ALL5_CARMA
38	6	100.0	7	1	ALL7_CVDPO
39	6	100.0	7	1	CCF1_ENTFA
40	6	100.0	7	1	CIA_ENTFA
41	6	100.0	7	1	DEM_PHYHY
42	6	100.0	7	1	FAF1_ASCSU
43	6	100.0	7	1	FAF2_ASCSU
44	6	100.0	7	1	FAF2_PANRE
45	6	100.0	7	1	FAR1_HELTI
46	6	100.0	7	1	FAR1_MACRS
47	6	100.0	7	1	FAR1_PROCL
48	6	100.0	7	1	FAR2_PROCL
49	6	100.0	7	1	FAR3_HAECO
50	6	100.0	7	1	FAR3_PANRE
51	6	100.0	7	1	FAR4_PANRE
52	6	100.0	7	1	FAR5_HIRME
53	6	100.0	7	1	FARB_CALVO
54	6	100.0	7	1	HY7_FIG
55	6	100.0	7	1	IPYR_CANAL
56	6	100.0	7	1	PPH2_LYCES
57	6	100.0	7	1	TVS1_LITRU
58	6	100.0	7	1	UN06_PINPS
59	6	100.0	7	2	Q15903_HUMAN
60	6	100.0	7	2	O98866_SPIOL
61	6	100.0	7	2	P82445_TOBAC
62	6	100.0	7	2	O34028_9SPHN
63	6	100.0	7	2	O8KMS9_GENTR
64	6	100.0	7	2	O07354_SYNP8
65	6	100.0	7	2	Q8K3H6_RAT
66	6	100.0	7	2	Q9YQ10_GCDRO
67	6	100.0	8	1	AKHG_GRYBI
68	6	100.0	8	1	AKH_LIBAU
69	6	100.0	8	1	AKH_PROTE
70	6	100.0	8	1	AKH_ROMMI
71	6	100.0	8	1	AKH_TABAT
72	6	100.0	8	1	ALL12_CARMA
73	6	100.0	8	1	ALL15_CARMA
74	6	100.0	8	1	ALL17_CARMA
75	6	100.0	8	1	ALL18_CARMA
76	6	100.0	8	1	ALL1_CVDPO
77	6	100.0	8	1	ALL3_CVDPO
78	6	100.0	8	1	ALL4_CVDPO
79	6	100.0	8	1	ALL5_CVDPO
80	6	100.0	8	1	ALL6_CVDPO
81	6	100.0	8	1	ALL7_CVDPO
82	6	100.0	8	1	ALL8_CVDPO
83	6	100.0	8	1	ALL9_CVDPO
84	6	100.0	8	1	ANGT2_BOTUA
85	6	100.0	8	1	CAD1_ENTFA
86	6	100.0	8	1	CCRN_DASVI
87	6	100.0	8	1	CCRN_MACBU
88	6	100.0	8	1	COX6B_RAT
89	6	100.0	8	1	CPD1_ENTFA
90	6	100.0	8	1	FAR1_PANRE
91	6	100.0	8	1	FAR1_PENMO
92	6	100.0	8	1	FAR2_MACRS
93	6	100.0	8	1	FAR3_HOMAM
94	6	100.0	8	1	FAR4_HOMAM
95	6	100.0	8	1	FAR4_MACRS
96	6	100.0	8	1	FAR7_ASCSU
97	6	100.0	8	1	FAR8_CALVO
98	6	100.0	8	1	HTF1_BUOR
99	6	100.0	8	1	
100	6	100.0	8	1	

ALIGNMENTS

P41491	locusta mig
P84005	penaeus mon
P81805	carcinus ma
P81806	carcinus ma
P81807	carcinus ma
P81808	carcinus ma
P82158	cydia pomon
P20104	enterococcu
P11932	enterococcu
P84523	phyllomedus
P31889	ascaris suu
P67879	ascaris suu
P67880	panagrellus
P41871	helisoma tr
P83274	macrobrachi
P38499	procambarus
P38498	procambarus
P81298	haemochus
P41874	panagrellus
P41875	panagrellus
P42564	hirudo medi
P41866	calliphora
P01153	sus scrofa
P83777	candida alb
P83779	lycopersico
P82065	litoria rub
P81675	pinus pinas
Q15903	homo sapien
O98866	spinacia ol
P82445	nicotiana t
O34028	sphingomona
O8KMS9	enterobacte
O07354	synechococc
Q8K3H6	rattus norv
Q9YQ10	transmissib
P67785	gryllus bim
P25418	libellula a
P61856	protophormi
P67786	romalea mic
P14595	tabanua atr
P81815	carcinus ma
P81818	carcinus ma
P81820	carcinus ma
P81821	carcinus ma
P82152	cydia pomon
P82154	cydia pomon
P41840	calliphora
P82155	cydia pomon
P41841	calliphora
P82156	cydia pomon
P82157	cydia pomon
P81809	carcinus ma
P81811	carcinus ma
P81812	carcinus ma
Q10582	bothrops ja
P13268	enterococcu
P68125	dasyurus vi
P68126	macropus eu
P80430	rattus norv
P13269	enterococcu
P41872	panagrellus
P83316	penaeus mon
P83275	macrobrachi
P41486	homarus ame
P41487	homarus ame
P83277	macrobrachi
P43171	ascaris suu
P41863	calliphora
P84261	blatta orie

```

RESULT 1
ACH1 ACHFU          STANDARD;          PRT;          4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6550;
RN [1]
RN PROTEIN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RP STRAIN=Perussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Perussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RN CHARACTERIZATION.
RP STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RN CRYSTALLIZATION.
RP MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-
RT Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
RT residue.";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -|- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
CC and produces a spike broadening of the identified heart excitatory
CC neuron (PON); also enhances the amplitude and frequency of the
CC heart beat. Has also an effect on several other muscles.
CC -----
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CC removed.
CC -----
DR PIR; A32480;
KW D-amino acid; Direct 2
FT MOD_RES 2
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 2 F 2

RESULT 2
FAR3_HIRME          STANDARD;          PRT;          4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hirudo medicinalis (Medicinal leech).
OS Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RN PROTEIN SEQUENCE.
RP MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
DR PIR; A32480;
KW D-amino acid; Direct 2
FT MOD_RES 2
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 2 F 2

RESULT 3
FAR4_HIRME          STANDARD;          PRT;          4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RN PROTEIN SEQUENCE.
RP MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC use as long as its content is in no way modified and this statement is not
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CC -----
KW MOD_RES 4
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 4 F 4

FMRFamide-like neuropeptide YLRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RN PROTEIN SEQUENCE.
RP MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC -----
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CC -----
KW MOD_RES 4
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 4 F 4

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RT trivolis";
RL Peptides 15:31-36(1994).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amidation; Direct protein sequencing; Neuropeptide.
KW MOD_RES 4 4 Phenylalanine amide.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 6
FLRF_HIRME STANDARD; PRT; 4 AA.
AC P69137; P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBI_TaxID=6421;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amidation; Direct protein sequencing; Neuropeptide.
KW MOD_RES 4 4 Phenylalanine amide.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
DB 1 F 1

RESULT 7
FLRF_HELTI STANDARD; PRT; 4 AA.
AC P69138; P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE FLRFamide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
NCBI_TaxID=27815;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE=Kidney;
TX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma

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DE Antho-RNAmide.  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
RN NCBI\_TaxID=6110;  
RX  
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.  
RX MEDLINE=90319122; PubMed=1973541;  
RA Grimelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,  
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;  
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Ans-NH2 (Antho-RNAmide), a sea  
RT anemone neuropeptide containing an unusual amino-terminal blocking  
RT group.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuron specific.  
CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref. 1.  
CC  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC PIR: A35779; A35779.  
DR Amidation; Direct protein sequencing; Neuropeptide.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 1 1 3-phenyllactic acid.  
FT MOD RES 4 4 Asparagine amide.  
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;  
  
Query Match 100.0%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 F 1  
Db 1 F 1  
  
RESULT 8  
FMRP HELTI  
ID FMRP HELTI STANDARD; PRT; 4 AA.  
AC P69148; P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE FMRPamide.  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeolidae; Planorbidae; Helisoma.  
OX NCBI\_TaxID=27815;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRPamide-related peptides from the kidney of the snail, Helisoma  
RT trivolvis.";  
RL Peptides 15:31-36 (1994).  
CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
CC activities include augmentation, induction, and regularization of  
CC cardiac contraction.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)  
CC family.  
CC  
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CC removed.  
CC  
CC Amidation; Direct protein sequencing; Neuropeptide.

FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
  
Query Match 100.0%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 F 1  
Db 1 F 1  
  
RESULT 9  
FMRP HIRME  
ID FMRP HIRME STANDARD; PRT; 4 AA.  
AC P69147; P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE FMRPamide.  
OS Hirudo medicinalis (Medicinal leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.  
RN NCBI\_TaxID=6421;  
OX [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;  
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
RT "Identification of Rfamide neuropeptides in the medicinal leech.";  
RL Peptides 12:897-908 (1991).  
CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
CC activities include augmentation, induction, and regularization of  
CC cardiac contraction.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)  
CC family.  
CC  
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CC removed.  
CC  
CC Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
  
Query Match 100.0%; Score 6; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 F 1  
Db 1 F 1  
  
RESULT 10  
FMRP MACNI  
ID FMRP MACNI STANDARD; PRT; 4 AA.  
AC P69145; P01162;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE FMRPamide (Peak C) (Cardioexcitatory neuropeptide).  
OS Macrocallista nimbosa (Sun-ray clam).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
OC Veneroidea; Veneridae; Macrocallista.  
OX NCBI\_TaxID=6594;  
RN [1]  
RP PROTEIN SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Cerebral pedal, and Visceral ganglion;  
RX MEDLINE=77215956; PubMed=877582;  
RA Price D.A., Greenberg M.J.;

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RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [2]
RP PROTEIN SEQUENCE, AND CHARACTERIZATION.
RX TISSUE=Ganglion;
RC MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
  from the central ganglia of a bivalve mollusc.";
RL Prep. Biochem. 7:261-281(1977).
CC -1- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
CC activities include augmentation, induction, and regularization of
CC cardiac contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A01426; ECVK.
DR AMidation; Direct protein sequencing; Neuropeptide.
KW MOD RES 4 4 4 Phenylalanine amide.
FT MOD RES 4 AA; 600 MW; 69D40699A0000000 CRC64;
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 12
FYRI_ANCEL STANDARD; PRT; 4 AA.
ID AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;
RA McFarlane I.D., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones; the unusual,
  biologically active L-3-phenylacetyl-Tyr-Arg-Ile-NH2.";
RL Phenylacetyl fragment Tyr-Arg-Ile-NH2.";
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
  inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
CC -----
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CC removed.
CC -----
CC KW Amidation; Direct protein sequencing; Neuropeptide.
FT PEPTIDE 1 4 Antho-Riamide I.
FT PEPTIDE 2 4 Antho-Riamide II.
FT MOD RES 1 1 3-phenylacetic acid.
FT MOD RES 4 4 Isoleucine amide.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1
Db 1 F 1

RESULT 13
OCPI_OCTMI STANDARD; PRT; 4 AA.
ID AC P58678;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.

```

```

OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP PROTEIN SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RC MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less active
CC than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.
CC
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CC
CC D-amino acid; Direct protein sequencing; Hormone.
KW MOD RES 2 2 D-phenylalanine (in form Ocp-1).
FT SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;
SQ
Query Match 100.0%; Score 6; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 2 F 2
RESULT 14
Q16047 HUMAN
ID Q16047 HUMAN PRELIMINARY; PRT; 4 AA.
AC Q16047;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 2 receptor alpha-subunit (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92062171; PubMed=1840490;
RA Mercken L., Moras V., Hemon L., Lionne B., Bousseau A.,
RA Dautry-Varot A., Collins M., Mayaux J.F.;
RT "An exon 5-deleted mRNA encodes a functional interleukin 2 receptor
RT alpha-subunit.";
RL Biochem. Biophys. Res. Commun. 180:1390-1395(1991).
DR EMBL; S64248; AAB20279.1; -; mRNA.
DR HSSP; P01112; 1PLL.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON TER 4 4
SQ SEQUENCE 4 AA; 525 MW; 69CAB769A0000000 CRC64;
Query Match 100.0%; Score 6; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 1 F 1

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RESULT 15
ALL14 CARMA
ID ALL14 CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinus maenas.
DE Carcinus maenas.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Fortunoidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
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CC
CC Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
KW MOD RES 5 5 Leucine amide (potential).
FT SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
SQ
Query Match 100.0%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 3 F 3
RESULT 16
EI03 LITRU
ID EI03 LITRU STANDARD; PRT; 5 AA.
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Electrin-3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin glands.
CC
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CC -----  
 CC Anidation; Amphibian defense peptide; Direct protein sequencing.  
 FT MOD\_RES 5 5 Methionine amide.  
 SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 1 F 1

## RESULT 17

E104 LITRU  
 ID E104 LITRU STANDARD; PRT; 5 AA.  
 AC P82100;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Electrin-4.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OC NCBI\_TaxID=104895;  
 RN [1]

PROTEIN SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella".  
 RL Aust. J. Chem. 52:639-645(1999).

CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.  
 CC -----  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC Anidation; Amphibian defense peptide; Direct protein sequencing.  
 FT MOD\_RES 5 5 Histidine amide.  
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 1 F 1

## RESULT 18

FARP-ARTTR  
 ID FARP-ARTTR STANDARD; PRT; 5 AA.  
 AC P41853;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRamide-like neuropeptide RYRF-amide.  
 OS Artiposthia triangulata (New Zealand flatworm).  
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;  
 OC Terricola; Geoplanidae; Arthurdendyus.  
 OC NCBI\_TaxID=132421;  
 RN [1]

RP PROTEIN SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=942111927; PubMed=7909164; DOI=10.1016/0167-0115(94)90189-9;  
 RA Maulie A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;  
 RT "RYRFamide: a turbellarian FMRamide-related peptide (FARP).";  
 RL Regul. Pept. 50:37-43(1994).  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.

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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.

CC Anidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 5 5 Phenylalanine amide.  
 SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 5 F 5

## RESULT 19

FARP-CHICK  
 ID FARP-CHICK STANDARD; PRT; 5 AA.  
 AC P83308;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRamide-like neuropeptide (LPLRF-amide).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]

PROTEIN SEQUENCE, AND SYNTHESIS.

RC TISSUE=Brain;  
 RX PubMed=6137771;  
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;  
 RT "A novel active pentapeptide from chicken brain identified by  
 RT antibodies to FMRamide.";

RL Nature 305:328-330(1983).  
 CC -1- FUNCTION: May function as a neurotransmitter or modulator.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 CC family.

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 CC removed.

CC Anidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 5 5 Phenylalanine amide.  
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 F 1  
 |  
 Db 5 F 5



DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 01-FEB-2005 (Rel. 46, Last annotation update)  
DE Rubellidin-3.1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylodae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT 'The structure of new peptides from the Australian red tree frog  
RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
RT of evolutionary trends of amphibians.';  
RL Aust. J. Chem. 49:955-963(1996).  
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
CC activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -1- MASS SPECTROMETRY: MW=655; METHOD=MS; RANGE=1-5; NOTE=Ref.1.  
CC  
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CC  
CC Amidation; Amphibian defense peptide; Direct protein sequencing.  
KW MOD\_RES 5 Threonine amide.  
FT  
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;  
Query Match 100.0%; Score 6; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 3 F 3  
RESULT 24  
ID RBE32\_LITRU STANDARD; PRT; 5 AA.  
AC P82073;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 01-FEB-2005 (Rel. 46, Last annotation update)  
DE Rubellidin-3.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylodae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP PROTEIN SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT 'Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.';  
RL Aust. J. Chem. 52:639-645(1999).  
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
CC activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC  
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CC  
KW Amphibian defense peptide; Direct protein sequencing.  
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;  
Query Match 100.0%; Score 6; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 3 F 3  
RESULT 25  
ID SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P19991;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Subesophageal ganglion pentapeptide.  
OS Acheta domesticus (House cricket).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Acheta.  
OX NCBI\_TaxID=6997;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Wicker C., Wicker C.;  
RT 'Isolation and structure of a peptide isolated from the subesophageal  
RT ganglion of Acheta domesticus (orthoptera).';  
RL Comp. Biochem. Physiol. 88C:185-187(1987).  
CC -1- SUBCELLULAR LOCATION: Main peptide from the subesophageal  
CC ganglia.  
CC  
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CC  
CC PIR; JS0319; JS0319.  
KW Direct protein sequencing.  
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;  
Query Match 100.0%; Score 6; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 F 1  
Db 5 F 5  
RESULT 26  
ID TPIS\_CANPA STANDARD; PRT; 5 AA.  
AC P54714;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate  
DE isomerase) (Fragment).  
GN NamesPili;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP PROTEIN SEQUENCE.  
RT TISSUE=Heart;  
RX MEDLINE=98163340; PubMed=9504812;

RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -|- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone  
 CC phosphate.  
 CC -|- PATHWAY: Plays an important role in several metabolic pathways.  
 CC -|- SUBUNIT: Homodimer (By similarity).  
 CC -|- SIMILARITY: Belongs to the triosephosphate isomerase family.  
 CC -----  
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 CC -----  
 CC HSC-2DPAGE; P54714; DOG.  
 DR InterPro: IPR000652; Triophos\_ismrse.  
 DR PROSITE; PS00171; TIM; PARTIAL.  
 KW Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis;  
 KW Glycolysis; Isomerase; Lipid synthesis; Pentose shunt.  
 FT NON\_TER 1 1  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;  
 Query Match 100.0%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 1 F 1  
 -----  
 RESULT 27  
 UC22\_MAIZE  
 ID UC22\_MAIZE STANDARD; PRT; 5 AA.  
 AC P80628;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 474)  
 DE (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.1, its MW is: 30.4 kDa.  
 CC -----  
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 CC -----  
 CC Maize-2DPAGE; P80628; COLEOPTILE.  
 DR Granele; P80628; -.  
 DR MaizeDB; 123954; -.  
 KW Direct protein sequencing.  
 FT NON\_TER 1 1  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 100.0%; Score 6; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 2 F 2  
 -----  
 RESULT 28  
 CIP1\_MYTE  
 ID CIP1\_MYTE STANDARD; PRT; 6 AA.  
 AC P13736;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Contraction-inhibiting peptide I (MIP I).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -|- FUNCTION: Inhibitory action on contractions in several molluscan  
 CC muscles.  
 CC -|- SIMILARITY: To M.edulis MIP II.  
 CC -----  
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 CC -----  
 CC PIR; A27696; A27696.  
 KW Amidation; Direct protein sequencing; Hormone.  
 MOD\_RES 6 Valine amide.  
 FT SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;  
 Query Match 100.0%; Score 6; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 F 1  
 DB 5 F 5  
 -----  
 RESULT 29  
 CIP2\_MYTE  
 ID CIP2\_MYTE STANDARD; PRT; 6 AA.  
 AC P13737;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-2005 (Rel. 46, Last annotation update)  
 DE Contraction-inhibiting peptide II (MIP II).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP PROTEIN SEQUENCE.  
 RC TISSUE=Pedal ganglion;  
 RX MEDLINE=88240357; PubMed=3377776;  
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;  
 RT "Structures and actions of Mytilus inhibitory peptides.";  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -|- FUNCTION: Inhibitory action on contractions in several molluscan  
 CC muscles.



```

CC -!- SIMILARITY: To M.edulis MIP I.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; B27696; B27696.
CC Amidation; Direct protein sequencing; Hormone.
CC MOD RES 6 Valine amide.
CC SEQUENCE 6 AA; 621 MW; 72C9C687DD81000 CRC64;
CC -----
Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 5 F 5
-----
RESULT 30
EI01 LITRU
ID EI01 LITRU STANDARD; PRT; 6 AA.
AC P82056;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Electrin-1.
OS Litoria rubella (Desert tree frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
CC Pelodyadinae; Litoria.
CC NCBI_TaxID=104895;
CC [1]
CC PROTEIN SEQUENCE.
CC TISSUE=Skin secretion;
CC Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
CC "Peptides from the skin glands of the Australian buzzing tree frog
CC Litoria electrica. Comparison with the skin peptides from Litoria
CC rubella.";
CC Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amidation; Amphibian defense peptide; Direct protein sequencing.
CC MOD RES 6 Methionine amide.
CC SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
CC -----
Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 1 F 1
-----
RESULT 31
FARP_MONEK
ID FARP_MONEK STANDARD; PRT; 6 AA.
AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide GNFRF-amide.

```

```

OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RN PROTEIN SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRamide: a novel FMRamide-immunoreactive peptide isolated from
RT the sheep tapeworm, Moniezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A43129; A43129.
CC Amidation; Direct protein sequencing; Neuropeptide.
CC MOD RES 6 Phenylalanine amide.
CC SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;
CC -----
Query Match 100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 3 F 3
-----
RESULT 32
LOK1 LOCM1
ID LOK1 LOCM1 STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
CC Acridoidea; Acrididae; Oedipodinae; Locusta.
CC NCBI_TaxID=7004;
CC [1]
CC PROTEIN SEQUENCE.
CC TISSUE=Corpora cardiaca;
CC MEDLINE=92262851; PubMed=1585017; DOI=10.1016/0167-0115(92)90063-Z;
CC Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
CC de Loof A.;
CC "Locustakinin, a novel myotropic peptide from Locusta migratoria,
CC isolation, primary structure and synthesis.";
CC Regul. Pept. 37:49-57(1992).
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A61068; A61068.
CC Amidation; Direct protein sequencing; Neuropeptide.
CC MOD RES 6 Glycine amide.
CC SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;
CC -----

```

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Query Match      100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      2 F 2

RESULT 33
PYF1_PENMO
ID PYF1_PENMO STANDARD; PRT; 6 AA.
AC P84005;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide tyrosine phenylalanine 1 (Pem-PYF1).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP PROTEIN SEQUENCE, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Eye stalk; DOI=10.1016/S0196-9781(02)00176-6;
RX PubMed=12431727; Pupum J., Krungkasem C., Longyant S., Panchan N.,
RA Chaiyuthangkura P., Sithigorngul W., Petsom A.;
RT "Four novel PYFs: members of NPX/PP peptide superfamily from the
eye stalk of the giant tiger prawn Penaeus monodon.";
RL Peptides 23.1895-1906(2002).
CC -!- FUNCTION: May act as a neurotransmitter, neuromodulator or
neurohormone.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Limited to neuronal cell bodies, neuronal
processes and sinus gland.
CC -!- MASS SPECTROMETRY: MW=801.5; METHOD=MALDI; RANGE=1-6; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the NPX family.
CC
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removed.
CC
CC InterPro; IPR001955; Pancreatic hormn.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; PARTIAL.
DR PROSITE; PS0276; PANCREATIC_HORMONE_2; PARTIAL.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 6 6 Phenylalanine amide (Potential).
SQ SEQUENCE 6 AA; 802 MW; 69D417740DC46000 CRC64;

Query Match      100.0%; Score 6; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      6 F 6

RESULT 34
ALL2_CARMA
ID ALL2_CARMA STANDARD; PRT; 7 AA.
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinustatin-2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.

Query Match      100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      5 F 5

RESULT 35
ALL3_CARMA
ID ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinustatin-3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
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removed.
CC
CC Direct protein sequencing; Multigene family; Neuropeptide.
SQ SEQUENCE 7 AA; 796 MW; 672879CDB476B70 CRC64;

Query Match      100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      5 F 5

NCBI_TaxID=6759;
[1]
PROTEIN SEQUENCE.
TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
"Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the allatostatin family.
-----
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removed.
-----
Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
MOD_RES 7 7 Leucine amide (Potential).
SEQUENCE 7 AA; 770 MW; 672879CDB5DDB70 CRC64;

Query Match      100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      5 F 5

Query Match      100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 F 1
Db      5 F 5

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```

Db          5 F 5
-----
RESULT 36
ALL4_CARMA
ID ALL4_CARMA STANDARD; PRT; 7 AA.
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinus maenas
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
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removed.
CC
CC Direct protein sequencing; Multigene family; Neuropeptide.
KW
FT MEDLINE=98121193; PubMed=9461295;
RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
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removed.
CC
CC Direct protein sequencing; Multigene family; Neuropeptide.
KW
SQ SEQUENCE 7 AA; 782 MW; 672879CDBC476AC0 CRC64;
Query Match 100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 5 F 5
-----
RESULT 37
ALL5_CARMA
ID ALL5_CARMA STANDARD; PRT; 7 AA.
AC P81808;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Carcinus maenas
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
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removed.
CC
CC Direct protein sequencing; Multigene family; Neuropeptide.
KW
SQ SEQUENCE 7 AA; 782 MW; 672879CDBC476AC0 CRC64;
Query Match 100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 5 F 5
-----
RESULT 38
ALL7_CVDPO
ID ALL7_CVDPO STANDARD; PRT; 7 AA.
AC P82158;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cydia pomonella
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Larva;
RC MEDLINE=98054539; PubMed=9392829; DOI=10.1016/S0196-9781(97)00188-5;
RX Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309 (1997).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the allatostatin family.
CC
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removed.
CC
CC Direct protein sequencing; Neuropeptide.
KW
FT MOD_RES 7 7
SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;
Query Match 100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 F 1
Db 5 F 5
-----
RESULT 39
CCF1_ENTFA
ID CCF1_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

```

Search completed: February 18, 2006, 08:00:56  
Job time : 94.9474 secs

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OX  NCBI_TaxID=1351;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=89008313; PubMed=3139658;
RA  Mori M., Sakagami Y., Iehi Y., Isogai A., Kitada C., Fujino M.,
RA  Adsit J.C., Dunny G.M., Suzuki A.;
RT  "Structure of cCF10, a peptide sex pheromone which induces conjugative
RT  transfer of the Streptococcus faecalis tetracycline resistance
RT  plasmid, pCF10.";
RL  J. Biol. Chem. 263:14574-14578(1988).
CC  -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
CC  hemolysin plasmid pCF10.
CC  -----
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CC  -----
CC  PIR; A30812; A30812.
KW  Direct protein sequencing; Pheromone.
SQ  SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match      100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 F 1
DB      6 F 6

RESULT 40
ID_  CIA_ENTFA      STANDARD;      PRT;      7 AA.
AC  P11332;
DT  01-OCT-1989 (Rel. 12, Created)
DT  01-OCT-1989 (Rel. 12, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS  Enterococcus faecalis (Streptococcus faecalis).
OC  Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX  NCBI_TaxID=1351;
RN  [1]
RP  PROTEIN SEQUENCE.
RX  MEDLINE=87005252; PubMed=3093276; DOI=10.1016/0014-5793(86)81342-4;
RA  Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA  White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT  "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT  CAM373.";
RL  FEBS Lett. 206:69-72(1986).
CC  -!- FUNCTION: CAM373 induces mating response of donor cells harboring
CC  pAM373.
CC  -!- MISCELLANEOUS: The N-terminus is possibly responsible for
CC  specificity of pheromones to plasmids.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
CC  PIR; A25269; A25269.
KW  Direct protein sequencing; Pheromone.
SQ  SEQUENCE 7 AA; 734 MW; 75BDD7205C05DB0 CRC64;

Query Match      100.0%; Score 6; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 F 1
DB      3 F 3
```

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OM protein - protein search, using sw model

Run on: February 18, 2006, 07:51:13 ; Search time 197.053 Seconds  
(without alignments)  
46.545 Million cell updates/sec

Title: US-09-868-131C-48

Perfect score: 54

Sequence: 1 XTFCGTXXYXPE 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 05.80:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	98.1	308	Q515Y9	ENTHI
2	53	98.1	420	Q51G39	ENTHI
3	53	98.1	518	Q9SEG2	MAIZE
4	53	98.1	685	Q76850	CALVI
5	52	96.3	201	Q817M6	CAEL
6	52	96.3	314	Q8MQE2	CAEL
7	52	96.3	428	Q60947	TRYCR
8	52	96.3	559	Q61511	CAEBR
9	52	96.3	581	Q8MQE3	CAEL
10	52	96.3	617	Q8MQE4	CAEL
11	52	96.3	646	SK2	SCHPO
12	52	96.3	683	Q6C936	YARLI
13	52	96.3	690	Q8NKP8	CRYNV
14	52	96.3	696	SK1	SCHPO
15	52	96.3	699	Q59ST4	CANAL
16	52	96.3	711	Q75BF3	ASHGO
17	52	96.3	734	Q6CWJ5	KLULA
18	52	96.3	746	Q6FTT2	CANGA
19	52	96.3	751	Q6BUB2	DEBHA
20	52	96.3	753	Q4PH11	USTWA
21	52	96.3	767	Q6FK01	CANGA
22	52	96.3	781	Q6BSR0	DEBHA
23	52	96.3	787	Q5AHG6	CANAL
24	52	96.3	813	Q6CKF2	KLULA
25	52	96.3	817	Q5K7C2	CRYNE
26	52	96.3	819	Q55HT7	CRYNE
27	52	96.3	821	RAD53	YEAST
28	52	96.3	821	Q6B1S1	YEAST
29	52	96.3	823	SCH	YEAST
30	52	96.3	837	Q75CE9	ASHGO
31	52	96.3	875	Q4WJD1	ASPERGILLUS

32	52	96.3	896	2	Q4IQN6	GIBZE
33	52	96.3	898	2	Q6C079	YARLI
34	52	96.3	903	2	Q52GN5	MAGR
35	52	96.3	911	2	Q7SGW9	NEUCR
36	52	96.3	917	2	Q9HGS0	BOTCI
37	52	96.3	919	2	Q5B5E2	EMENI
38	52	96.3	919	2	Q8N1K8	EMENI
39	52	96.3	1210	2	Q4P998	USTMA
40	52	96.3	1216	2	Q8N1W8	USTMA
41	51	94.4	69	2	Q39300	BRANA
42	51	94.4	69	2	Q39301	BRANA
43	51	94.4	69	2	Q39302	BRANA
44	51	94.4	221	2	Q00603	XENLA
45	51	94.4	272	2	Q8SRL5	ENCUC
46	51	94.4	293	2	Q6NXX3	MOUSE
47	51	94.4	312	2	Q5HZB1	RAT
48	51	94.4	351	2	Q9CST0	MOUSE
49	51	94.4	368	2	Q7QJ74	ANOXA
50	51	94.4	422	2	Q4RKC0	TETNG
51	51	94.4	451	2	Q7Z721	HUMAN
52	51	94.4	460	1	CD51	SCHPO
53	51	94.4	465	2	Q4T8X6	TETNG
54	51	94.4	471	2	Q6GNN5	XENLA
55	51	94.4	482	1	KS6B2	HUMAN
56	51	94.4	482	2	Q9BR50	HUMAN
57	51	94.4	483	2	Q9FJ55	ARATH
58	51	94.4	484	2	Q9QGB3	ARTSF
59	51	94.4	485	1	KS6B2	MOUSE
60	51	94.4	489	2	Q9SN43	ARATH
61	51	94.4	490	2	Q94533	DROME
62	51	94.4	501	2	Q6DCH1	XENLA
63	51	94.4	501	2	Q9W6Y9	XENLA
64	51	94.4	502	2	O22971	ARATH
65	51	94.4	502	2	Q5ZLW5	CHICK
66	51	94.4	502	2	Q802Y7	BRARE
67	51	94.4	508	2	Q68Y49	ORYSA
68	51	94.4	508	2	Q9SLZ6	ORYSA
69	51	94.4	511	2	Q5QNM6	ORYSA
70	51	94.4	516	2	Q84XC0	PEA
71	51	94.4	520	2	Q7F595	ORYSA
72	51	94.4	520	2	Q9LP51	ARATH
73	51	94.4	520	2	Q9SLZ5	ORYSA
74	51	94.4	522	2	Q9BMX7	APLCA
75	51	94.4	525	1	KS6B1	HUMAN
76	51	94.4	525	1	KS6B1	MOUSE
77	51	94.4	525	1	KS6B1	RABIT
78	51	94.4	525	1	KS6B1	RAT
79	51	94.4	525	2	Q4R519	MACFA
80	51	94.4	525	2	Q5SWG1	MOUSE
81	51	94.4	525	2	Q6P2Z5	XENTR
82	51	94.4	526	2	Q41592	WHEAT
83	51	94.4	540	2	Q61BU7	CAEBR
84	51	94.4	540	2	Q5JLUS2	ORYSA
85	51	94.4	540	2	Q535V4	AEDAE
86	51	94.4	580	2	Q9NAH6	CAEL
87	51	94.4	637	2	P91656	DROME
88	51	94.4	851	2	Q4IAJ4	GIBZE
89	51	94.4	879	2	Q21694	CAEL
90	51	94.4	884	2	Q5B121	EMENI
91	51	94.4	890	2	Q4WND7	ASPFU
92	51	94.4	1123	2	Q7S434	NEUCR
93	51	94.4	65	2	Q643X2	CANFA
94	50	92.6	79	2	Q4TEY1	TETNG
95	50	92.6	87	2	P79347	BOVIN
96	50	92.6	87	2	Q4T906	TETNG
97	50	92.6	87	2	Q4T906	TETNG
98	50	92.6	119	2	Q6NGY9	9BLO
99	50	92.6	125	2	Q5NDF4	HYDEC
100	50	92.6				

ALIGNMENTS

RESULT 1  
 Q515Y9\_ENTHI  
 ID Q515Y9\_ENTHI PRELIMINARY; PRT; 308 AA.  
 AC Q515Y9;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Protein kinase, putative.  
 GN ORFNames=64.t00038;  
 OS Entamoeba histolytica HM-1:IMSS  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 NCBI\_TaxID=294381;  
 RX NUCLEOTIDE SEQUENCE.  
 RP [1]  
 RC STRAIN=HM-1:IMSS;  
 RA Loftus B., Anderson I., Davies R., Almark U.C., Samuelson J.,  
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
 RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,  
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
 RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
 RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
 RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,  
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
 RA Fraser C.M., Hall N.;  
 RA NCBI\_TaxID=294381;  
 RL Nature 433:865-868(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL: AAFB01000244; EAL48681.1; -; Genomic\_DNA.  
 CC GO: GO:0016301; F\_kinase activity; IEA.  
 CC InterPro: IPR000961; Pkinase C.  
 CC InterPro: IPR000719; Prot\_kinase.  
 CC InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
 CC InterPro: IPR002290; Ser\_thr\_pkin\_AS.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam: PF00069; Pkinase; I.  
 CC Pfam: PF00433; Pkinase; I.  
 CC ProDom: PD000001; Prot\_kinase; 1.  
 CC SMART: SM00233; PH; 1.  
 CC SMART: SM00133; S\_TK\_X; 1.  
 CC SMART: SM00220; S\_TK; 1.  
 CC SMART: SM00219; TyRK; 1.  
 CC PROSITE: PS50003; PH DOMAIN; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE: PS500108; PROTEIN\_KINASE\_ST; 1.  
 KW Kinase.  
 SQ SEQUENCE 308 AA; 35211 MW; 63CB03D5510D1F4C CRC64;  
 Query Match 98.1%; Score 53; DB 2; Length 308;  
 Best Local Similarity 75.0%; Pred. No. 0.03;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXYXAPE 13  
 DB 144 TFCGTAAYLAPE 155  
 ||||| |||||  
 RESULT 2  
 Q51G39\_ENTHI  
 ID Q51G39\_ENTHI PRELIMINARY; PRT; 420 AA.  
 AC Q51G39;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Protein kinase, putative.  
 GN ORFNames=3.t00144;  
 OS Entamoeba histolytica HM-1:IMSS.  
 OC Eukaryota; Entamoebidae; Entamoeba.  
 NCBI\_TaxID=294381;  
 RX NUCLEOTIDE SEQUENCE.  
 RP [1]  
 RC STRAIN=HM-1:IMSS;  
 RA Loftus B., Anderson I., Davies R., Almark U.C., Samuelson J.,  
 RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
 RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
 RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,  
 RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
 RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
 RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
 RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
 RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,  
 RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
 RA Fraser C.M., Hall N.;  
 RA NCBI\_TaxID=294381;  
 RL Nature 433:865-868(2005).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL: AAFB01000244; EAL48681.1; -; Genomic\_DNA.  
 CC GO: GO:0016301; F\_kinase activity; IEA.  
 CC InterPro: IPR000961; Pkinase C.  
 CC InterPro: IPR000719; Prot\_kinase.  
 CC InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
 CC InterPro: IPR002290; Ser\_thr\_pkin\_AS.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam: PF00069; Pkinase; I.  
 CC Pfam: PF00433; Pkinase; I.  
 CC ProDom: PD000001; Prot\_kinase; 1.  
 CC SMART: SM00133; S\_TK\_X; 1.  
 CC SMART: SM00220; S\_TK; 1.  
 CC SMART: SM00219; TyRK; 1.  
 CC PROSITE: PS50003; PH DOMAIN; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE: PS500108; PROTEIN\_KINASE\_ST; 1.  
 KW Kinase.  
 SQ SEQUENCE 420 AA; 48372 MW; 579BCE674AA810D9 CRC64;  
 Query Match 98.1%; Score 53; DB 2; Length 420;  
 Best Local Similarity 75.0%; Pred. No. 0.044;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXYXAPE 13  
 DB 256 TFCGTAAYLAPE 267  
 ||||| |||||  
 RESULT 3  
 Q9SEG2\_MAIZE  
 ID Q9SEG2\_MAIZE PRELIMINARY; PRT; 518 AA.  
 AC Q9SEG2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Protein kinase PK4.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 NCBI\_TaxID=4577;  
 RX NUCLEOTIDE SEQUENCE.  
 RP [1]  
 RC MEDLINE=20239027; PubMed=10778756; DOI=10.1007/s004380051179;  
 RA Ohba H., Steward N., Kawasaki S., Berberich T., Ikeda Y., Koizumi N.,  
 RA Kusano T., Sano H.;  
 RT "Diverse response of rice and maize genes encoding homologs of WPK4,  
 RT an SNF1-related protein kinase from wheat, to light, nutrients, low  
 RT temperature and cytokinins.";  
 RL Mol. Gen. Genet. 263:359-366(2000).  
 RL [1]

CC -!- FUNCTION: CIPK serine-threonine protein kinases interact with CBL  
 CC proteins. Binding of a CBL protein to the regulatory NAF domain of  
 CC CIPK protein lead to the activation of the kinase in a calcium-  
 CC dependent manner (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL: AF141378; AAF22219.1; -; mRNA.  
 DR HSSP: P49137; INXK.  
 DR Gramene: Q9SEG2; -.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR GO: GO:0007165; P:signal transduction; IEA.  
 DR InterPro: IPR004041; NAF.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam: PF03822; NAF; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00220; S\_TK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 518 AA; 57242 MW; 96ED3F76B5684BA1 CRC64;

Query Match 98.1%; Score 53; DB 2; Length 518;  
 Best Local Similarity 75.0%; Pred. No. 0.054;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
 |||||  
 DB 203 TFCGTAAYVAPE 214

RESULT 4  
 O76850 CALVI PRELIMINARY; PRT; 685 AA.  
 AC O76850;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Eye-specific protein kinase C.  
 GN Name=inac homolog;  
 OS Calliphora vicina (Blue blowfly) (Calliphora erythrocephala).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=7373;  
 [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Retina.  
 RX MEDLINE=96421251; PubMed=8823935; DOI=10.1016/1011-1344(96)07310-1;  
 RA Huber A., Sander P., Wollrath U., Groell C., Gerdon G., Paulsen R.;  
 RT "Isolation of genes encoding photoreceptor-specific proteins by  
 RT immunoscreening with antibodies directed against purified blowfly  
 RT rhodopsin";  
 RT J. Photochem. Photobiol. B 35:69-76 (1996).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Retina;  
 RA Huber A., Sander P., Baehner M., Paulsen R.;  
 RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ005377; CAA06507.1; -; mRNA.  
 DR HSSP: P05696; IDSJ.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0007242; P:intracellular signaling cascade; IEA.  
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR000008; C2.

DR InterPro: IPR002219; DAG\_PE-bind.  
 DR InterPro: IPR000961; Pkinase C.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam: PF00130; C1\_1; 2.  
 DR Pfam: PF00168; C2; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR Pfam: PF00433; Pkinase C; 1.  
 DR PRINTS: PR00360; C2DOMAIN.  
 DR PRINTS: PR00008; DAGPEDOMAIN.  
 DR SMART: SM00109; C1; 2.  
 DR SMART: SM00239; C2; 1.  
 DR SMART: SM00220; S\_TK; 1.  
 DR SMART: SM00133; S\_TK\_X; 1.  
 DR PROSITE: PS00499; C2\_DOMAIN\_1; 1.  
 DR PROSITE: PS50004; C2\_DOMAIN\_2; 1.  
 DR PROSITE: PS00479; DAG\_PE\_BIND\_DOM\_1; 2.  
 DR PROSITE: PS50081; DAG\_PE\_BIND\_DOM\_2; 2.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Kinase.  
 SQ SEQUENCE 685 AA; 78036 MW; E493A9F033F99A7A CRC64;

Query Match 98.1%; Score 53; DB 2; Length 685;  
 Best Local Similarity 75.0%; Pred. No. 0.071;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
 |||||  
 DB 513 TFCGTSYYVAPE 524

RESULT 5  
 Q8I7M6 CAEEL PRELIMINARY; PRT; 201 AA.  
 AC Q8I7M6;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein C09G4.2;  
 GN ORFNames=C09G4.2;  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Bristol N2;  
 RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;  
 RG The C. elegans sequencing consortium;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology";  
 RL Science 282:2012-2018 (1998).  
 DR EMBL: U42438; AAN84875.1; -; Genomic\_DNA.  
 DR HSSP: P31751; LMRV.  
 DR Ensembl: C09G4.2; Caenorhabditis elegans.  
 DR WormBase: WBGene00015650; C09G4.2.  
 DR WormPep: C09G4.2d; CE32576.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro: IPR002374; CGMP\_kin.  
 DR InterPro: IPR000961; Pkinase C.  
 DR InterPro: IPR000719; Prot\_kinase.  
 DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR ProDom: PD000001; Prot\_kinase; 1.  
 DR SMART: SM00133; S\_TK\_X; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Complete proteome; Hypothetical protein.

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SQ SEQUENCE 201 AA; 23083 MW; EFCCAAGF5662D9BE CRC64;
Query Match 96.3%; Score 52; DB 2; Length 201;
Best Local Similarity 75.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
|||||
Db 49 TFCGTAEYVAPE 60

RESULT 6
O8MQE2_CABEL
ID Q8MQE2_CABEL PRELIMINARY; PRT; 314 AA.
AC Q8MQE2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein C09G4.2.
GN ORFNames=C09G4.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; U42438; AAM75370.1; -; Genomic_DNA.
DR HSSP; P31751; 1GZK.
DR Ensembl; C09G4.2; Caenorhabditis elegans.
DR WormBase; WBGene00015650; C09G4.2.
DR WormPep; C09G4.2b; CEJ1157.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0064674; P:protein kinase activity; IEA.
DR InterPro; IPR002374; CGMP kin.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR000961; Pkinase_C.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Complete proteome; Hypothetical protein; Kinase;
KW Nucleotide-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 314 AA; 35903 MW; 2108905B3F183D19 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 314;
Best Local Similarity 75.0%; Pred. No. 0.053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
|||||
Db 162 TFCGTAEYVAPE 173

RESULT 7
O60947_TRYCR
ID O60947_TRYCR PRELIMINARY; PRT; 428 AA.
AC O60947;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rac serine-threonine kinase homolog.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;

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OC Schizotrypanum.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tulahuen 2;
RX MEDLINE=99404823; PubMed=10477173; DOI=10.1016/S0166-6851(99)00076-6;
RA Pascucci V., Labriola C., Tellez-Inon M.T., Parodi A.J.;
RT "Molecular and biochemical characterization of a protein kinase B from
RT Trypanosoma cruzi.";
RL Mol. Biochem. Parasitol. 102:21-33(1999).
DR EMBL; U63742; AAC08427.1; -; Genomic_DNA.
DR HSSP; P31751; 1GZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Kinase.
SQ SEQUENCE 428 AA; 48548 MW; 4762B9DC74E2AD59 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 428;
Best Local Similarity 75.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
|||||
Db 260 TFCGTAEYVAPE 271

RESULT 8
Q615L1_CAEBR
ID Q615L1_CAEBR PRELIMINARY; PRT; 559 AA.
AC Q615L1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG15634 (Fragment).
GN Name=CBG15634;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBSJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC EMBL; CAACO1000074; CAB69446.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008603; F:cAMP-dependent protein kinase complex; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002373; CAMP_kin.
DR InterPro; IPR000595; CNMP_binding.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase_AS.

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DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00027; CNMP binding; 1.  
DR Pfam: PF00069; Pkinase; 1.  
DR PRINTS: PR00103; CAMPKINASE.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00100; CNMP; 1.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TKG; 1.  
DR SMART: SM00219; TyK; 1.  
DR PROSITE: PS00888; CNMP BINDING\_1; 1.  
DR PROSITE: PS00889; CNMP BINDING\_2; 1.  
DR PROSITE: PS00442; CNMP BINDING\_3; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00108; PROTEIN KINASE\_ST; 1.  
DR Complete proteome; Hypothetical protein.  
SQ SEQUENCE 559 AA; 64265 MW; B95952BC5F79561 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 559;  
Best Local Similarity 75.0%; Pred. No. 0.092;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 407 TFCGTAAYVAPE 418

RESULT 9  
Q8MQE3 CAEBL  
ID Q8MQE3 CAEBL PRELIMINARY; PRT; 581 AA.  
AC Q8MQE3;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Hypothetical protein C09G4.2;  
GN ORFNames=C09G4.2;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RT The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; U42438; AAM753369.1; -; Genomic\_DNA.  
DR HSSP; P49137; INXK.  
DR Ensembl; C09G4.2; Caenorhabditis elegans.  
DR WormBase; WBGene00015650; C09G4.2.  
DR WormPep; C09G4.2a; CE31156.  
DR GO; GO:0005952; F:ATP binding; IEA.  
DR GO; GO:0005524; F:CAMP-dependent protein kinase complex; IEA.  
DR GO; GO:0008603; F:CAMP-dependent protein kinase regulator act...; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR002373; CAMP kin.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR000961; Pkinase\_C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00027; CNMP binding; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00103; CAMPKINASE.  
DR SMART; SM00100; CNMP; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR PROSITE; PS00888; CNMP BINDING\_1; 1.  
DR PROSITE; PS00889; CNMP BINDING\_2; 1.  
DR PROSITE; PS00442; CNMP BINDING\_3; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
DR Complete proteome; Hypothetical protein.  
SQ SEQUENCE 581 AA; 70852 MW; 0261DC699241D38A CRC64;

Query Match 96.3%; Score 52; DB 2; Length 617;  
Best Local Similarity 75.0%; Pred. No. 0.1;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 429 TFCGTAAYVAPE 440

RESULT 10  
Q8MQE4 CAEBL  
ID Q8MQE4 CAEBL PRELIMINARY; PRT; 617 AA.  
AC Q8MQE4;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Hypothetical protein C09G4.2;  
GN ORFNames=C09G4.2;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RT The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; U42438; AAM753371.1; -; Genomic\_DNA.  
DR HSSP; P49137; INXK.  
DR Ensembl; C09G4.2; Caenorhabditis elegans.  
DR WormBase; WBGene00015650; C09G4.2.  
DR WormPep; C09G4.2c; CE31158.  
DR GO; GO:0005952; F:ATP binding; IEA.  
DR GO; GO:0005524; F:CAMP-dependent protein kinase complex; IEA.  
DR GO; GO:0008603; F:CAMP-dependent protein kinase regulator act...; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR002373; CAMP kin.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR000961; Pkinase\_C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00027; CNMP binding; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00103; CAMPKINASE.  
DR SMART; SM00100; CNMP; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR PROSITE; PS00888; CNMP BINDING\_1; 1.  
DR PROSITE; PS00889; CNMP BINDING\_2; 1.  
DR PROSITE; PS00442; CNMP BINDING\_3; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
DR Complete proteome; Hypothetical protein.  
SQ SEQUENCE 617 AA; 70852 MW; 0261DC699241D38A CRC64;

Query Match 96.3%; Score 52; DB 2; Length 617;  
Best Local Similarity 75.0%; Pred. No. 0.1;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 429 TFCGTAAYVAPE 440

DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00027; CNMP binding; 1.  
DR Pfam: PF00069; Pkinase; 1.  
DR PRINTS: PR00103; CAMPKINASE.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00100; CNMP; 1.  
DR SMART: SM00133; S\_TK\_X; 1.  
DR SMART: SM00220; S\_TKG; 1.  
DR SMART: SM00219; TyK; 1.  
DR PROSITE: PS00888; CNMP BINDING\_1; 1.  
DR PROSITE: PS00889; CNMP BINDING\_2; 1.  
DR PROSITE: PS00442; CNMP BINDING\_3; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE: PS0011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR Complete proteome; Hypothetical protein.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 581 AA; 67013 MW; 3744C6D77C64C9A9 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 581;  
Best Local Similarity 75.0%; Pred. No. 0.096;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 407 TFCGTAEYVAPE 418

RESULT 9  
Q8MQE3 CAEBL  
ID Q8MQE3 CAEBL PRELIMINARY; PRT; 581 AA.  
AC Q8MQE3;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Hypothetical protein C09G4.2;  
GN ORFNames=C09G4.2;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RT The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; U42438; AAM75337.1; -; Genomic\_DNA.  
DR HSSP; P49137; INXK.  
DR Ensembl; C09G4.2; Caenorhabditis elegans.  
DR WormBase; WBGene00015650; C09G4.2.  
DR WormPep; C09G4.2C; CE31158.  
DR GO; GO:0005952; C:AMP-dependent protein kinase complex; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008603; F:AMP-dependent protein kinase regulator act.; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR002373; CAMP kin.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00027; CNMP binding; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00103; CAMPKINASE.  
DR SMART; SM00100; CNMP; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR PROSITE; PS00888; CNMP BINDING\_1; 1.  
DR PROSITE; PS00889; CNMP BINDING\_2; 1.  
DR PROSITE; PS00442; CNMP BINDING\_3; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS0011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR Complete proteome; Hypothetical protein.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 559 AA; 64265 MW; B95952BC5F79561 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 559;  
Best Local Similarity 75.0%; Pred. No. 0.092;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 407 TFCGTAEYVAPE 418

RESULT 9  
Q8MQE3 CAEBL  
ID Q8MQE3 CAEBL PRELIMINARY; PRT; 581 AA.  
AC Q8MQE3;  
DT 01-OCT-2002 (TREMBlrel. 22, Created)  
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE Hypothetical protein C09G4.2;  
GN ORFNames=C09G4.2;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RT The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; U42438; AAM75337.1; -; Genomic\_DNA.  
DR HSSP; P49137; INXK.  
DR Ensembl; C09G4.2; Caenorhabditis elegans.  
DR WormBase; WBGene00015650; C09G4.2.  
DR WormPep; C09G4.2a; CE31156.  
DR GO; GO:0005952; C:AMP-dependent protein kinase complex; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0008603; F:AMP-dependent protein kinase regulator act.; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR002373; CAMP kin.  
DR InterPro; IPR000595; CNMP binding.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00027; CNMP binding; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00103; CAMPKINASE.  
DR SMART; SM00100; CNMP; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKG; 1.  
DR PROSITE; PS00888; CNMP BINDING\_1; 1.  
DR PROSITE; PS00889; CNMP BINDING\_2; 1.  
DR PROSITE; PS00442; CNMP BINDING\_3; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS0011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR Complete proteome; Hypothetical protein.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 559 AA; 64265 MW; B95952BC5F79561 CRC64;

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QY      2 TFCGTXXYXAPE 13
DB      465 TFCGTAEYVAPE 476

RESULT 11
ID      SCK2_SCHPO STANDARD; PRT; 646 AA.
AC      Q10364;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Serine/threonine-protein kinase sck2 (EC 2.7.1.37).
GN      Name=sck2; ORFNames=SPAC22E12.14c;
OS      Schizosaccharomyces pombe (Fission yeast).
OC      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC      Schizosaccharomycetales; Schizosaccharomycetaceae;
OC      Schizosaccharomycetes.
OX      NCBI_TaxID=4896;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=972;
RX      MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA      Wood V., Gwilliam R., Rejandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA      Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA      Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA      Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA      Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA      Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jacobs K.,
RA      James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA      Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA      Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
RA      Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA      Skelton J., Simmonds M.N., Squares R., Stevens K.,
RA      Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA      Woodward J.R., Volkert G., Aert R., Robben J., Grymonprez B.,
RA      Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA      Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
RA      Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA      Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA      Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA      Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA      Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA      Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA      Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA      Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA      Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT      "The genome sequence of Schizosaccharomyces pombe.";
RL      Nature 415:871-880(2002).
RN      [2]
RP      FUNCTION.
RX      MEDLINE=98228264; PubMed=9560431;
RA      Fujita M., Yamamoto M.;
RT      "S. pombe sck2", a second homologue of S. cerevisiae SCH9 in fission
RT      yeast, encodes a putative protein kinase closely related to PKA in
RT      function.";
RT      Curr. Genet. 33:248-254(1998).
CC      -!- FUNCTION: Protein kinase that is part of growth control pathway
CC      which is at least partially redundant with the cAMP pathway.
CC      -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC      -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PKC
CC      subfamily.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; Z70043; CAA93901.1; -; Genomic_DNA.
CC      DR      PIR; T38171; T38171.
CC      DR      HSP; P31751; 1GZK.

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GeneDB Spombe; SPAC22E12.14c; --

GO; GO:0019933; P:G-protein-mediated signaling; IMP.

GO; GO:0046999; P:regulation of conjugation; IGI.

InterPro; IPR002110; ANK.

InterPro; IPR000961; Pkinase C.

InterPro; IPR000719; Prot Kinase.

InterPro; IPR008271; Ser\_Thr\_kinase.

InterPro; IPR002290; Ser\_Thr\_kinase.

Pfam; PF00069; Pkinase; 1.

Pfam; PF00433; Pkinase C; 1.

PRINTS; PR01415; ANKYRIN.

ProDom; PD000001; Prot Kinase; 1.

SMART; SM00133; S\_TK\_X; 1.

SMART; SM00220; S\_TK; 1.

PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.

PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

ATP-binding; Complete proteome; Kinase; Nucleotide-binding;

KW Serine/threonine-protein kinase; Transferase.

FT DOMAIN 266 527 Protein kinase.

FT NP\_BIND 272 280 ATP (By similarity).

FT ACT\_SITE 392 392 Proton acceptor (By similarity).

FT BINDING 295 295 ATP (By similarity).

SQ SEQUENCE 646 AA; 71899 MW; 4F37BF7FD8C56FF CRC64;

Query Match 96.3%; Score 52; DB 1; Length 646;

Best Local Similarity 75.0%; Pred. No. 0.11;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13

DB 426 TFCGTTDYLAPE 437

RESULT 12

Q6C936 YARLI PRELIMINARY; PRT; 683 AA.

AC Q6C936;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Yarrowia lipolytica chromosome D of strain CLIB99 of Yarrowia

DE lipolytica.

GN OrderedLocustNames=YALJ014542g;

OS Yarrowia lipolytica (Candida lipolytica).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Dipodascaceae; Yarrowia.

OX NCBI\_TaxID=4952;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=1529592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,

RA Goffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

RA Boissarie A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Nicaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

RA Swennen D., Tekala F., Wesolowski-Louvel M., Weithof E., Wirth B.,

RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,

RA Wincker P., Souciet J.-L.;

RT "Genome evolution in yeasts.";

RL Nature 430:35-44(2004).

DR EMBL; CR392130; CAG81014.1; -; Genomic\_DNA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr pkinase.  
 DR InterPro; IPR008271; Ser Thr pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00168; C2; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS50004; C2 DOMAIN 2; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Complete proteome.  
 KW Complete proteome.  
 SQ SEQUENCE 683 AA; 76060 MW; 7A1B286610F05ECA CRC64;

Query Match 96.3%; Score 52; DB 2; Length 683;  
 Best Local Similarity 75.0%; Pred. No. 0.11; Mismatches 0; Gaps 0;  
 Matches 9; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |||||  
 DB 470 TFCGTTTEYLAPE 481

RESULT 13  
 Q8NKF8 CRYNV  
 ID Q8NKF8 CRYNV PRELIMINARY; PRT; 690 AA.  
 AC Q8NKF8; 22, Created  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Protein kinase Sch9.  
 GN Name=Sch9;  
 OS Cryptococcus neoformans var. grubii (Filobasidiella neoformans var. grubii).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
 ON NCBI\_TaxID=178876;  
 RX NUCLEOTIDE SEQUENCE.  
 RP STRAIN=H99;  
 RA Wang P., Cox G.M., Heitman J.;  
 RT "A Sch9 protein kinase homologue controlling virulence independently of the cAMP pathway in Cryptococcus neoformans.";  
 RL Curr. Genet. 46:247-255(2004).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AF430213; AAM21494.1; -; Genomic\_DNA.  
 DR HSSP; P49137; INXK.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004574; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser Thr pkin\_AS.  
 DR InterPro; IPR002290; Ser Thr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 690 AA; 76468 MW; B35566E563BDB3B20 CRC64;  
 Query Match 96.3%; Score 52; DB 2; Length 690;  
 Best Local Similarity 75.0%; Pred. No. 0.11; Mismatches 0; Gaps 0;  
 Matches 9; Conservative 0; Indels 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXYXAPE 13  
 ||||| |||||  
 DB 413 TFCGTTTEYLAPE 424

RESULT 14  
 SCK1 SCHPO  
 ID SCK1 SCHPO STANDARD; PRT; 696 AA.  
 AC P50570; Q9JTF3;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Serine/threonine-protein kinase sck1 (EC 2.7.1.37).  
 GN Name=sck1; ORFNames=SPAC1B9.02C;  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 ON NCBI\_TaxID=4896;  
 RX NUCLEOTIDE SEQUENCE.  
 RP STRAIN=972;  
 RA Wood V., Gilliam R., Rajadream M.A., Lyne M.H., Lyne R., Stewart A., Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G., Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K., James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moulé S., Mungall K.L., Murphy L.D., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J.R., Volkert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Calbert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Daga R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RN Nature 415:871-880(2002).  
 RP FUNCTION.  
 RX MEDLINE=97388592; PubMed=9245826;  
 RA Soto T., Fernandez J., Cansado J., Vicente-Soler J., Gacto M.;  
 RT "Protein kinase Sck1 is involved in trehalase activation by glucose and nitrogen source in the fission yeast Schizosaccharomyces pombe." Microbiology 143:2457-2463(1997).  
 CC -1- FUNCTION: Protein kinase that is part of growth control pathway which is at least partially redundant with the cAMP pathway.

```
CC      Required for trehalase activation.
CC      -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family. cAMP
CC      subfamily.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; D38108; BAA07286.1; -; Genomic DNA.
CC      EMBL; AL10953; CAB53053.1; -; Genomic DNA.
CC      F1R; S55694; S55694.
CC      HSPB; P31751; IGZK.
CC      GeneDB Spombe; SPAC1B9.02c; -.
CC      GO; GO:0019333; P:cAMP-mediated signaling; IMP.
CC      InterPro; IPR000008; C2.
CC      InterPro; IPR000961; Pkinase_C.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR008271; Ser_thr_pkin_AS.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00168; C2; 1.
CC      Pfam; PF00069; Pkinase; 1.
CC      Pfam; PF00433; Pkinase_C; 1.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM00239; C2; 1.
CC      SMART; SM00133; S_TK_X; 1.
CC      SMART; SM00220; S_TK; 1.
CC      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC      PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
CC      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC      ATP-binding; cAMP; Complete proteome; Kinase; Nucleotide-binding;
KW      Serine/threonine-protein kinase; Transferase.
FT      DOMAIN 302 563 Protein kinase.
FT      NP_BIND 308 316 ATP (By similarity).
FT      ACT_SITE 428 428 Proton acceptor (By similarity).
FT      BINDING 331 331 ATP (By similarity).
FT      CONFLICT 199 199 A -> R (in Ref. 1).
SQ      SEQUENCE 696 AA; 78595 MW; A7B05F5EED42AF7 CRC64;

Query Match          96.3%; Score 52; DB 1; Length 696;
Best Local Similarity 75.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXXKPE 13
DB      462 TFCGTEYLKPE 473

RESULT 15
Q59ST4 CANAL
ID Q59ST4 CANAL PRELIMINARY; PRT; 699 AA.
AC Q59ST4.
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Likely protein kinase.
GN Name=RAD53; ORFNames=CaO19.14198, CaO19.6936;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;
RX STRAIN=SC5314.
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.
RT "The diploid genome sequence of Candida albicans."
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
```

```
RP      NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000148; EAK93529.1; -; Genomic DNA.
DR EMBL; AACQ01000147; EAK93566.1; -; Genomic DNA.
SQ      SEQUENCE 699 AA; 78292 MW; B98C49BC2BD0BCE9 CRC64;

Query Match          96.3%; Score 52; DB 2; Length 699;
Best Local Similarity 75.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXXKPE 13
DB      331 TFCGTLAYKPE 342

RESULT 16
Q75BF3 ASHGO
ID Q75BF3 ASHGO PRELIMINARY; PRT; 711 AA.
AC Q75BF3.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ADL389WP.
GN Name=ADL389W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307(2004).
DR EMBL; AE016817; AASS1531.1; -; Genomic DNA.
DR HSP; Q63450; 1A06.
DR AGD; ADL389W; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS00004; C2_DOMAIN_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Complete proteome.
SQ      SEQUENCE 711 AA; 80515 MW; EC6E6404CABEE81B CRC64;

Query Match          96.3%; Score 52; DB 2; Length 711;
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Best Local Similarity 75.0%; Pred. No. 0.12; Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||  
DB 462 TFCGTTTEYLAPE 473

## RESULT 17

Q6CWJ5\_KLUJLA  
ID Q6CWJ5\_KLUJLA PRELIMINARY; PRT; 734 AA.  
AC Q6CWJ5;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome B of strain NRRL Y-1140 of Kluyveromyces lactis.  
GN OrderedLocusNames=KLLA0B03586g;  
OS Kluyveromyces lactis (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.  
OX NCBI\_TaxID=28985;  
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E., V.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykaaten C.,  
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrast A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.;  
RT "Genome evolution in yeasts.";

RL Nature 430:35-44(2004).

RL EMBL; CR382122; CAH02087.1; -; Genomic\_DNA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR000961; Pkinase C.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002230; Ser Thr\_pkinase.

DR InterPro; IPR008271; Ser Thr\_pkin\_AS.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00433; Pkinase C; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00239; C2; 1.

DR SMART; SM00220; S\_TK; 1.

DR SMART; SM00133; S\_TK\_X; 1.

DR SMART; SM00219; Tyr\_K; 1.

DR PROSITE; PS50004; C2 DOMAIN 2; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50004; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW Complete proteome.

SQ SEQUENCE 734 AA; 82341 MW; DB9A39CBA2E2B888 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 734;

Best Local Similarity 75.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||

DB 483 TFCGTTTEYLAPE 494

## RESULT 18

Q6FTT2\_CANGA  
ID Q6FTT2\_CANGA PRELIMINARY; PRT; 746 AA.  
AC Q6FTT2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Candida glabrata strain CBS138 chromosome F complete sequence.  
GN OrderedLocusNames=CAGL0F09075g;  
OS Candida glabrata (Yeast) (Torulopsis glabrata).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5478;  
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX STRAIN=ATCC 2001 / CBS 138;

RX PubMed=15229592; DOI=10.1038/nature02579;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E., V.,

RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykaaten C.,

RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,

RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,

RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

RA Kerrast A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,

RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,

RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,

RA Wincker P., Souciet J.-L.;

RT "Genome evolution in yeasts.";

RL Nature 430:35-44(2004).

RL EMBL; CR380952; CAG59286.1; -; Genomic\_DNA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000008; C2.

DR InterPro; IPR000961; Pkinase C.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR002230; Ser Thr\_pkinase.

DR InterPro; IPR008271; Ser Thr\_pkin\_AS.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00168; C2; 1.

DR Pfam; PF00069; Pkinase; 1.

DR Pfam; PF00433; Pkinase C; 1.

DR PRINTS; PR00360; C2DOMAIN.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00239; C2; 1.

DR SMART; SM00220; S\_TK; 1.

DR SMART; SM00133; S\_TK\_X; 1.

DR SMART; SM00219; Tyr\_K; 1.

DR PROSITE; PS50004; C2 DOMAIN 2; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW Complete proteome.

SQ SEQUENCE 746 AA; 83800 MW; 99F3EB0024522187 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 746;

Best Local Similarity 75.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||

DB 498 TFCGTTTEYLAPE 509

## RESULT 19

Q6BUB2\_DEBHA  
ID Q6BUB2 DEBHA PRELIMINARY; PRT; 751 AA.  
AC Q6BUB2  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DE Hypothetical protein.  
GN ORFNames=UM00602.1;  
OS Ustilago maydis 521.  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=237631;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=521;  
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,  
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavsky L.,  
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
RA David R., Dawot T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
RA Finkbeiner A., Goyette A., Graham J., Grandbois E., Gyatsen K., Hafez N.,  
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kanat A., Kanvyaselis M., Karlsson E.,  
RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Lindblad-toh K., Liu X., Lokiytsang T., Lokiytsang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Maneus L.,  
RA Mesirov J., Mihalev A., Mihova T., Mikkeleen T., Mlenga V., Moru K.,  
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okaowo O., O'leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schubach R., Seaman C., Settupalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnev C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,  
RA Towse S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,  
RA Zimmer A., Zody M., Lander E.  
RT "The genome sequence of Ustilago maydis."  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAC001000013; EMBL1251.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 753 AA; 82966 MW; B632346998EE43C CRC64;  
Query Match 96.3%; Score 52; DB 2; Length 753;  
Best Local Similarity 75.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXYXAPE 13  
|||||  
DB 285 TFCGTLAYVAPE 296  
RESULT 20  
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ID Q4PH11\_USTMA  
AC Q4PH11  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DE Hypothetical protein.  
GN ORFNames=UM00602.1;  
OS Ustilago maydis 521.  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=237631;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=521;  
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
RA Arachchi H., Armbruster J., Bachantang P., Baldwin J., Barry A.,  
RA Bayul T., Blitshteyn B., Bloom T., Blye J., Boguslavsky L.,  
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,  
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RA David R., Dawot T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
RA Finkbeiner A., Goyette A., Graham J., Grandbois E., Gyatsen K., Hafez N.,  
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RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
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RA Kells C., Kieu A., Kisher P., Kodira C., Kulbokas E., Labutti K.,  
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RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schubach R., Seaman C., Settupalli S., Sharpe T.,  
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RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
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RA Towse S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
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RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembek L.,  
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RT "The genome sequence of Ustilago maydis."  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAC001000013; EMBL1251.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 753 AA; 82966 MW; B632346998EE43C CRC64;  
Query Match 96.3%; Score 52; DB 2; Length 753;  
Best Local Similarity 75.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXYXAPE 13  
|||||  
DB 285 TFCGTLAYVAPE 296  
RESULT 20  
Q4PH11\_USTMA PRELIMINARY; PRT; 753 AA.  
ID Q4PH11\_USTMA  
AC Q4PH11  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DE Hypothetical protein.  
GN ORFNames=UM00602.1;  
OS Ustilago maydis 521.  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
OX NCBI\_TaxID=237631;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=521;  
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
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RA Finkbeiner A., Goyette A., Graham J., Grandbois E., Gyatsen K., Hafez N.,  
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RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kanat A., Kanvyaselis M., Karlsson E.,  
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RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
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RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Maneus L.,  
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RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okaowo O., O'leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schubach R., Seaman C., Settupalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnev C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stenson K., Stone C., Stone S., Stubbs M., Tal

DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)  
 DE Candida glabrata strain CBS138 chromosome M complete sequence.  
 GN OrderedLocusNames=CAGL0M02233g;  
 OC Candida glabrata (Yeast) (Torulopsis glabrata).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5478;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 2001 / CBS 138;  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Marck C., Neuveglise C., Tallia E.,  
 RA Lafontaine I., de Montigny J., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boirame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,  
 RA Despons L., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; CR380959; CAG62419.1; -; Genomic\_DNA.  
 DR SMR; Q6PK01; 4-156, 548-705.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000253; FHA.  
 DR InterPro; IPR0001245; Tyr\_kinase.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00498; FHA; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000004; Prot\_kinase; 1.  
 DR SMART; SM00240; FHA; 2.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00219; TyrK; 1.  
 DR PROSITE; PS00006; FHA DOMAIN; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Autophagy; Complete proteome; Kinase; Nucleotide-binding;  
 KW Protein transport; Serine/threonine-protein kinase; Transferase;  
 KW Transport.  
 SQ SEQUENCE 767 AA; 86732 MW; AF6CE2ADADC268F2 CRC64;  
 Query Match 96.3%; Score 52; DB 2; Length 767;  
 Best Local Similarity 75.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 TFCGTXXXAPE 13  
 DB 344 TFCGLTAYVAPE 355  
 RESULT 22  
 Q6BSR0 DEBHA  
 ID Q6BSR0 DEBHA PRELIMINARY; PRT; 781 AA.  
 AC Q6BSR0;  
 DT 25-OCT-2004 (TremBLrel. 28, Created)  
 DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)  
 DE Similar to Candida albicans CA4227.

GN OrderedLocusNames=DEHA0D07601g;  
 OS Debaryomyces hansenii (Yeast) (Torulaspora hansenii).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.  
 OX NCBI\_TaxID=4959;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=ATCC 36239 / CBS 767;  
 RX PubMed=15229592; DOI=10.1038/nature02579;  
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
 RA Boirame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,  
 RA Despons L., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissbach J.,  
 RA Wincker P., Souciet J.-L.;  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; CR382136; CAG86904.1; -; Genomic\_DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF00168; C2; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00219; TyrK; 1.  
 DR PROSITE; PS50004; C2 DOMAIN 2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 781 AA; 87409 MW; 5DE2981F43D10228 CRC64;  
 Query Match 96.3%; Score 52; DB 2; Length 781;  
 Best Local Similarity 75.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 2 TFCGTXXXAPE 13  
 DB 544 TFCGTTEYLAPE 555  
 RESULT 23  
 Q5AHG6 CANAL  
 ID Q5AHG6 CANAL PRELIMINARY; PRT; 787 AA.  
 AC Q5AHG6;  
 DT 10-MAY-2005 (TremBLrel. 30, Created)  
 DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)  
 DE Potential cAMP-dependent protein kinase Sch9.  
 GN Name=Sch9; ORFNames=CaO19.829, CaO19.8449;  
 OS Candida albicans SC5314.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=237561;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-SC5314; DOI=10.1073/pnas.0401648101;
RX PubMed=15123810;
RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Izung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000019; EAL02133.1; -; Genomic_DNA.
DR EMBL; AACQ01000018; EAL02261.1; -; Genomic_DNA.
KW Kinase.
SQ SEQUENCE 787 AA; 88754 MW; F80278D9A0E50707 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 787;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYXKPE 13
DB 552 TFCGTXYXKPE 563

RESULT 24
Q6CKF2_KLULA
ID Q6CKF2_KLULA PRELIMINARY; PRT; 813 AA.
AC Q6CKF2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome F of strain NRRL Y-
DE 1140 of Kluyveromyces lactis.
OS Ordered locus names: KLLA0F11143g;
GN Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28995;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 / IFO 1267 / NRRL Y-1140 / WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durand P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
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DR EMBL; CR382126; CAG98295.1; -; Genomic_DNA.
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DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.

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DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00498; FHA; 2.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50006; FHA DOMAIN; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Autophagy; Complete proteome; Kinase; Nucleotide-binding;
KW Protein transport; Serine/threonine-protein kinase; Transferase;
KW Transport.
SQ SEQUENCE 813 AA; 91483 MW; 9499356992B8789E CRC64;

Query Match 96.3%; Score 52; DB 2; Length 813;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYXKPE 13
DB 348 TFCGTXYXKPE 359

RESULT 25
Q5K7C2_CRYNE
ID Q5K7C2_CRYNE PRELIMINARY; PRT; 817 AA.
AC Q5K7C2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Protein kinase Sch9, putative.
GN ORFNames=CN000360;
OS Cryptococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=JEC21;
RX PubMed=15533466; DOI=10.1126/science.1103773;
RA Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzyminski M.I.,
RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA Fraser C.M., Hyman R.W.;
RT "The genome of the basidiomycetous yeast and human pathogen
RT Cryptococcus neoformans.";
RL Science 307:1321-1324(2005).
DR EMBL; AE017356; AAW47041.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.

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DR InterPro: IPR008271; Ser thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00089; Pkinase_1.
DR Pfam: PF00433; Pkinase_C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK_C; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Complete proteome; Kinase
SQ SEQUENCE 817 AA; 88881 MW; 7125E1DBCDD90CC6C CRC64;

Query Match 96.3%; Score 52; DB 2; Length 817;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
Db 541 TFCGTTEYLAPE 552

RESULT 26
Q55HT7_CRYNE PRELIMINARY; PRT; 819 AA.
AC Q55HT7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNAMES=CNB0340;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AA001000066; EAL17206.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 819 AA; 89112 MW; 06DF2F7303F35FC2 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 819;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
Db 543 TFCGTTEYLAPE 554

RESULT 27
RAD53_YEAST
ID RAD53_YEAST STANDARD; PRT; 821 AA.
AC P22216;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase RAD53 (EC 2.7.1.37) (Serine-protein
DE Kinase 1).
GN Names=RAD53; Synonyms=MEC2, SAD1, SPK1; OrderedLocusNames=YPL153C;
GN ORFNAMES=P2588;
OS Saccharomyces cerevisiae (Baker's yeast).

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OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=91117267; PubMed=1899289;
RA Stern D.F., Zheng P., Beidler D.R., Zerillo C.;
RT "Spk1, a new kinase from Saccharomyces cerevisiae, phosphorylates
RT proteins on serine, threonine, and tyrosine.";
RL Mol. Cell. Biol. 11:987-1001(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=S288c / AB972;
RX MEDLINE=97103777; PubMed=8948103;
DOI=10.1002/(SICI)1097-0061(199611)12:14<1483::AID-YEA34>3.3.CO;2-F;
RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of 55 kb on the left arm of yeast chromosome XVI
RT identifies a small nuclear RNA, a new putative protein kinase and two
RT new putative regulators.";
RL Yeast 12:1483-1492(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288c / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoerge W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Brueckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., Dipaolo T., Dubois E., Dueterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
RA Hunnicke-Smith S., Hyman R.W., Johnston M., Kalman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle B., Rajandream M.A., Reckmann S.,
RA Rieger M., Riles L., Roberts D., Schaefer M., Scharfe M., Scherens B.,
RA Schramm S., Schroeder M., Sdicu A.-M., Tettelin H., Urrestarazu L.A.,
RA Ushinsky S., Vierendeels F., Viissers S., Voss H., Walsh S.V.,
RA Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.-W.,
RA Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105(1997).
RN [4]
RP FUNCTION, AND SUBCELLULAR LOCATION.
RX PubMed=8355715;
RA Zheng P., Fay D.S., Burton J., Xiao H., Pinkham J.L., Stern D.F.;
RT "SPK1 is an essential S-phase-specific gene of Saccharomyces
RT cerevisiae that encodes a nuclear serine/threonine/tyrosine kinase.";
RL Mol. Cell. Biol. 13:5829-5842(1993).
RN [5]
RP FUNCTION.
RX MEDLINE=95047382; PubMed=7958905;
RA Allen J.B., Zhou Z., Siede W., Friedberg E.C., Elledge S.J.;
RT "The SAD1/RAD53 protein kinase controls multiple checkpoints and DNA
RT damage-induced transcription in yeast.";
RL Genes Dev. 8:2401-2415(1994).
RN [6]
RP FUNCTION.
RX MEDLINE=20018334; PubMed=10550056; DOI=10.1126/science.286.5442.1166;
RA Sanchez Y., Bachant J., Wang H., Hu F., Liu D., Tetzlaff M.,
RA Elledge S.J.;
RT "Control of the DNA damage checkpoint by chk1 and rad53 protein
RT kinases through distinct mechanisms.";
RL Science 286:1166-1171(1999).
RN [7]
RP PHOSPHORYLATION.
RX MEDLINE=20031667; PubMed=10562568; DOI=10.1093/emboj/18.22.6561;
RA Pellucio A., Lucica C., Liberi G., Marini F., Lopes M., Plevani P.,
RA Romano A., Di Fiore P.P., Folini M.;
RT "Activation of Rad53 kinase in response to DNA damage and its effect
RT in modulating phosphorylation of the lagging strand DNA polymerase.";
RL EMBO J. 18:6561-6572(1999).

```

[8]  
 RP STRUCTURE BY NMR OF 573-730.  
 RX MEDLINE=20057864; PubMed=10588905; DOI=10.1006/jmbi.1999.3313;  
 RA Liao H., Byeon I.-J.L., Tsai M.-D.;  
 RT "Structure and function of a new phosphopeptide-binding domain  
 RT containing the FHA2 of Rad53.";  
 RJ J. Mol. Biol. 294:1041-1049(1999).  
 RN [9]  
 RP INVOLVEMENT IN PHOSPHORYLATION OF RPH1.  
 RX PubMed=11809875; DOI=10.1093/nar/30.3.643;  
 RA Kim E.M., Jang Y.K., Park S.D.;  
 RT "Phosphorylation of Rph1, a damage-responsive repressor of PHR1 in  
 RT Saccharomyces cerevisiae, is dependent upon Rad53 Kinase.";  
 RL Nucleic Acids Res. 30:643-648(2002).  
 CC -1- FUNCTION: Controls S-phase checkpoint as well as G1 and G2 DNA  
 CC damage checkpoints. Phosphorylates proteins on serine, threonine,  
 CC and tyrosine. Prevents entry into anaphase and mitotic exit after  
 CC DNA damage via regulation of the Polo kinase CDC5. Seems to be  
 CC involved in the phosphorylation of RPH1.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -1- SIMILARITY: Contains 2 FHA domains.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; M55623; AAA35070.1; -; Genomic DNA.  
 DR EMBL; X96770; CAA65568.1; -; Genomic DNA.  
 DR EMBL; Z73509; CAA97858.1; -; Genomic DNA.  
 DR EIR; A39616; A39616.  
 DR PDB; 1DMZ; NMR; A=573-730.  
 DR PDB; 1FHQ; NMR; A=573-730.  
 DR PDB; 1FHR; NMR; A=573-730.  
 DR PDB; 1G3G; NMR; A=2-164.  
 DR PDB; 1G6G; X-ray; A/B=29-155.  
 DR PDB; 1J4K; NMR; A=573-730.  
 DR PDB; 1J4L; NMR; A=573-730.  
 DR PDB; 1J4O; NMR; A=14-164.  
 DR PDB; 1J4P; NMR; A=14-164.  
 DR PDB; 1J4Q; NMR; A=14-164.  
 DR PDB; 1K2M; NMR; A=573-730.  
 DR PDB; 1K2N; NMR; A=573-730.  
 DR PDB; 1K3J; NMR; A=14-164.  
 DR PDB; 1K3N; NMR; A=14-164.  
 DR PDB; 1K3Q; NMR; A=14-164.  
 DR PDB; 1QU5; NMR; A=549-730.  
 DR IntAct; P22216; -.  
 DR GernOnline; 144135; -.  
 DR Ensembl; YPL153C; Saccharomyces cerevisiae.  
 DR SGD; S00006074; RAD53.  
 DR GO; GO:0005634; C:nucleus; IDA.  
 DR GO; GO:0004712; F:protein threonine/tyrosine kinase activity; IDA.  
 DR GO; GO:0006281; P:DNA repair; IMP.  
 DR GO; GO:0006139; P:nucleobase, nucleoside, nucleotide and nucl. . .; IGI.  
 DR InterPro; IPR000253; FHA.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00498; FHA; 2.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00240; FHA; 2.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS50006; FHA DOMAIN; 2.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW 3D-structure; ATP-binding; Cell cycle; Complete proteome; DNA damage;

KW Kinase; Nuclear protein; Nucleotide-binding; Phosphorylation; Repeat;  
 KW Serine/threonine-protein kinase; Transferase; Tyrosine-protein kinase.  
 FT DOMAIN 66 116  
 FT PHA 1.  
 FT DOMAIN 138 466  
 FT PHA 2.  
 FT NP\_BIND 601 664  
 FT ATP (By similarity).  
 FT ACT\_SITE 204 212  
 FT Proton acceptor.  
 FT BINDING 319 319  
 FT ATP (By similarity).  
 FT STRAND 227 227  
 FT STRAND 34 38  
 FT TURN 39 40  
 FT STRAND 46 48  
 FT STRAND 52 57  
 FT HELIX 62 69  
 FT STRAND 72 73  
 FT TURN 76 77  
 FT STRAND 82 83  
 FT TURN 89 94  
 FT STRAND 95 96  
 FT STRAND 99 103  
 FT STRAND 109 111  
 FT TURN 112 113  
 FT STRAND 114 115  
 FT TURN 118 119  
 FT STRAND 122 123  
 FT TURN 126 127  
 FT STRAND 129 132  
 FT TURN 134 135  
 FT HELIX 137 139  
 FT STRAND 141 147  
 FT STRAND 149 153  
 FT TURN 154 154  
 FT STRAND 158 582  
 FT TURN 584 585  
 FT STRAND 592 594  
 FT TURN 596 597  
 FT STRAND 601 604  
 FT TURN 607 608  
 FT STRAND 611 612  
 FT TURN 616 617  
 FT TURN 620 621  
 FT STRAND 623 630  
 FT STRAND 644 651  
 FT TURN 654 655  
 FT STRAND 657 659  
 Query Match 96.3%; Score 52; DB 1; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 0.13;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXYXAPE 13  
 |||||  
 Db 354 TFCGTLAYVAPE 365  
 RESULT 28  
 QB1S1 YEAST PRELIMINARY; PRT; 821 AA.  
 AC Q6B1S1;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE YPL153C.  
 GN Name=RAD53;  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_taxid=4932;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,  
 RA Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,  
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,  
 RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,

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RA LaBaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombination cloning system.";
RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY693009; AAT93028.1; -; Genomic_DNA.
DR SMR; Q6B1S1; 2-164.
DR Ensembl; YPL153C; Saccharomyces cerevisiae.
DR SGD; S00006074; RAD53.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00498; FHA; 2.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 2.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS50006; FHA DOMAIN; 2.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 821 AA; 91934 MW; AAB353DC7DF68119 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 821;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13
DB 354 TFCGTLAYVAPE 365

RESULT 29
SCH9_YEAST STANDARD; PRT; 823 AA.
AC P11792;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine/threonine-protein kinase SCH9 (EC 2.7.1.37).
GN Names=Sch9; Synonyms=KOM1; OrderedLocNames=YHR205W;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=88255839; PubMed=3290050;
RA Toda T., Cameron S., Sass P., Wigler M.;
RT "SCH9, a gene of Saccharomyces cerevisiae that encodes a protein
RT distinct from, but functionally and structurally related to, CAMP-
RT dependent protein kinase catalytic subunits.";
RL Genes Dev. 2:517-527(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=JR26-19D;
RA MEDLINE=93182531; PubMed=8442384;
di Biasi F., Carra E., de Vendittis E., Masturzo P., Burderi E.,
RA Lambrianoudaki I., Mirisola M.G., Seidita G., Fasano O.;
RT "The SCH9 protein kinase mRNA contains a long 5' leader with a small
RT open reading frame.";
RL Yeast 9:21-32(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favella A., Fulton L., Gattung S., Geisel C., Kirsten J.,

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RA Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis B.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
CC -!- FUNCTION: Protein kinase that is part of growth control pathway
CC which is at least partially redundant with the CAMP pathway.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ENZYME REGULATION: Activated by CAMP.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CAMP
CC subfamily.
CC -!- SIMILARITY: Contains 1 C2 domain.
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; X12560; CAA31073.1; -; Genomic_DNA.
CC EMBL; X57629; CAA40853.1; ALT_INIT; Genomic_DNA.
CC EMBL; U00029; AAB69735.1; -; Genomic_DNA.
CC PIR; S48986; S48986.
CC HSP; P31751; IGZK.
CC Germline; 139523; -.
CC Ensembl; YHR205W; Saccharomyces cerevisiae.
CC SGD; S00001248; SCH9.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
CC GO; GO:0004674; F:protein serine/threonine kinase activity; IGI.
CC GO; GO:0001324; P:age-dependent response to oxidative stress . . . IMP.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IGI.
CC GO; GO:0008361; P:regulation of cell size; IDA.
CC GO; GO:0001302; P:replicative cell aging; IMP.
CC InterPro; IPR000008; C2.
CC InterPro; IPR000961; Pkinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF0433; Pkinase_C; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00239; C2; 1.
CC SMART; SM00133; S_TK_X; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS50004; C2 DOMAIN; FALSE NEG.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC ATP-binding; CAMP; Complete proteome; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 319 360
FT DOMAIN 411 670
FT NP_BIND 417 425
FT COMPBIAS 226 266
FT ACT_SITE 537 537
FT BINDING 440 440
FT CONFLICT 365 365
FT CONFLICT 750 750
FT CONFLICT 823 AA; 91680 MW; BDSFE116D9CDA65D CRC64;
SQ SEQUENCE 823 AA; 91680 MW; BDSFE116D9CDA65D CRC64;

Query Match 96.3%; Score 52; DB 1; Length 823;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13
DB 569 TFCGTLAYVAPE 580

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RESULT 30
Q75CE9 ASHGO
ID Q75CE9 ASHGO PRELIMINARY; PRT; 837 AA.
AC Q75CE9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ACRI42WP.
GN Name=ACRI42W;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_taxid=33169;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
RT Saccharomyces cerevisiae genome.";
RL Science 304:304-307 (2004).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AE016816; AA551368.1; -; Genomic_DNA.
DR HSSP; P22216; 1X3Q.
DR AGD; ACRI42W; -.
DR GO; GO:005524; P:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00498; FHA; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 2.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50006; FHA DOMAIN; 2.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Autophagy; Complete proteome; Kinase; Nucleotide-binding;
KW Protein transport; Serine/threonine-protein kinase; Transferase;
KW Transport.
SQ SEQUENCE 837 AA; 93518 MW; DDB15B755394B627 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 837;
Best Local Similarity 75.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTGXXYXAPE 13
|||||
Db 373 TFCGTLAYVAPE 384

RESULT 31
Q4WJD1 ASPFU
ID Q4WJD1 ASPFU PRELIMINARY; PRT; 875 AA.
AC Q4WJD1;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE CAMP-dependent protein kinase-like, putative.
GN ORFNames=Afulg06400;
OS Aspergillus fumigatus Af293.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

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OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_taxid=330879;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=Af293;
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H. Stanley.,
RA Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA Majeros W.H., May G.S., Miller B.B., Mohamoud Y., Molina M., Monod M.,
RA Moujina I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,
RA Penalva M.A., Perte M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,
RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Sanchez M.,
RA Ronning C.M., Rutter S., Salzberg S.L., Seeger K., Squares R.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA Machida M., Hall N., Barrell B., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHF01000007; EAL88351.1; -; Genomic_DNA.
SQ SEQUENCE 875 AA; 96605 MW; 506B7C18D96D2B93 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 875;
Best Local Similarity 75.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTGXXYXAPE 13
|||||
Db 637 TFCGTTEYLAPE 648

RESULT 32
Q4IQN6 GIBZE
ID Q4IQN6 GIBZE PRELIMINARY; PRT; 896 AA.
AC Q4IQN6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG00472.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocromycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_taxid=229533;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nueba C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Diaz J.S., Dudge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kellis C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,

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RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
RA Rachupka A., Ramaamy U., Raymond C., Retta R., Rise C., Rogov P.,  
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,  
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,  
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,  
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
RA Lander E.;  
RT "Fusarium graminearum genome sequence";  
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC EMBL: AACW01000019; EAA68485.1; -; Genomic\_DNA.  
KW Hypothetical protein  
SQ SEQUENCE 896 AA; 98469 MW; 78BFAECCCF4ACOB CRC64;

Query Match 96.3%; Score 52; DB 2; Length 896;  
Best Local Similarity 75.0%; Pred. No. 0.14;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 650 TFCGTTEYLAPE 661

RESULT 33  
Q6C079\_YARLI PRELIMINARY; PRT; 898 AA.  
AC Q6C079;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Similar to DEHAOC13211g Debaryomyces hansenii.  
GN OrderedLocuNames=YALI0F270939;  
OS Yarrowia lipolytica (Candida lipolytica).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Dipodasaceae; Yarrowia.  
OX NCBI\_TaxID=4952;  
RN [1]  
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP STRAIN=CLIB 122 / E 150;  
RX PubMed=15229592; DOI=10.1038/nature02579;  
RA Lafontaine I., de Montigny J., March C., Neugeglise C., Talla E.,  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,  
RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller R.,  
RA Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,  
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.-L.;  
RT "Genome evolution in yeasts";  
RL Nature 430:35-44(2004).

CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL: CR382132; CAC78745.1; -; Genomic\_DNA.  
DR GO: 0005524; F:ATP binding; IEA.  
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: 0004713; F:protein-tyrosine kinase activity; IEA.  
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR000253; FHA.  
DR InterPro: IPR00719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00498; FHA; 2.  
DR Pfam: PF00069; Pkinase; 1.

DR ProDom; PD0000001; Prot\_kinase; 1.  
DR SMART; SM00240; FHA; 2;  
DR SMART; SM00220; S\_TKc; 1.  
DR SMART; SM00219; TyrKC; 1.  
DR PROSITE; PS00006; FHA DOMAIN; 2.  
DR PROSITE; PS00107; PROTEIN KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
KW ATP-binding; Autophagy; Complete\_protease; Kinase; Nucleotide-binding;  
KW Protein transport; Serine/threonine-protein kinase; Transferase;  
KW Transport.  
SQ SEQUENCE 898 AA; 100328 MW; 8C648FB95899D28E CRC64;

Query Match 96.3%; Score 52; DB 2; Length 898;  
Best Local Similarity 75.0%; Pred. No. 0.15;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 346 TFCGTWAYIAPE 357

RESULT 34  
Q52GN5\_MAGGR PRELIMINARY; PRT; 903 AA.  
AC Q52GN5;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=MG01251.4;  
OS Magnaporthe grisea 70-15.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.  
OX NCBI\_TaxID=242507;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=70-15;  
RA Birren B., Nuebaum C., Abebe A., Abouelleil A., Adekoya E.,  
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,  
RA Arachi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
RA Bayat T., Blitshstein B., Bloom T., Blye J., Boguslavsky L.,  
RA Borowsky M., Boukhaltier B., Brunache A., Butler J., Calixte N.,  
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,  
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,  
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,  
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,  
RA Fitzgerald M., Farina A., Faro S., Ferreira P., Fischer H.,  
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,  
RA Gierke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,  
RA Hagopian D., Hegos B., Hall J., Hatcher B., Heller A., Higgins H.,  
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,  
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson E.,  
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,  
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,  
RA Landlad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,  
RA Lui A., Ma L., J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
RA Manning J., Maraballa R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Meneus L.,  
RA Mesirov J., Mihalev A., Mihova T., Mikelsen T., Mieng V., Moru K.,  
RA Mezes J., Mihalov A., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piquani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
RA Ratta R., Richaudon S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,  
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuina P.,  
RA Tenzing P., Testaye S., Theodore J., Thoultsang Y., Topham K.,  
RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,

RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Lander E.;  
 RT "The genome sequence of Magnaporthe grisea";  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 (2)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=70-15;  
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 (3)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=70-15;  
 RA Zhu H., Blackmon B.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AACU01000018; EAA55600.1; -; Genomic\_DNA.  
 KW Hypothetical protein.  
 SQ SEQUENCE 903 AA; 99144 MW; 6DD697B62835132A CRC64;

Query Match 96.3%; Score 52; DB 2; Length 903;  
 Best Local Similarity 75.0%; Pred. No. 0.15;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXKPE 13  
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 DB 658 TFCGTEYLAPE 669

RESULT 35  
 Q7SGW9 NEUCR  
 ID Q7SGW9 NEUCR PRELIMINARY; PRT; 911 AA.  
 AC Q7SGW9;  
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=NCU03200.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=OR74A;  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J.J., Endrizzi M.,  
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
 RA Kamal M., Kamysellis M., Mauceli E., Bielke C., Rudd S., Friseman D.,  
 RA Krystofova S., Raemussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,  
 RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;  
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa";  
 RL Nature 0:0-0 (2003).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AABX01000007; EAA35064.1; -; Genomic\_DNA.  
 DR HSSP; P31751; IGZK.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004674; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR000961; Pkinase\_C.

DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00168; C2; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; P000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS0108; PROTEIN\_KINASE\_ST; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 911 AA; 100129 MW; F103338DFF867CE5 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 911;  
 Best Local Similarity 75.0%; Pred. No. 0.15;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXKPE 13  
 |||||  
 DB 666 TFCGTEYLAPE 677

RESULT 36  
 Q9HGS0 BOTCI  
 ID Q9HGS0 BOTCI PRELIMINARY; PRT; 917 AA.  
 AC Q9HGS0;  
 DT 01-MAR-2001 (T-EMBLrel. 16, Created)  
 DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)  
 DE CAMP-dependent protein kinase catalytic subunit.  
 GN Name=pka2;  
 OS Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
 OC Helotiales; Sclerotiniaceae; Botryotinia.  
 OX NCBI\_TaxID=40559;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=SAS56;  
 RA Schulze Gronover C., Klimpel A.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 (2)  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=SAS56;  
 RA Tudzynski B.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AJ290951; CAC03748.1; -; Genomic\_DNA.  
 DR HSSP; P31751; IGZK.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; P000001; Prot\_kinase; 1.  
 DR SMART; SM00239; C2; 1.  
 DR SMART; SM00133; S-TK\_X; 1.  
 DR SMART; SM00220; S-TK; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS0108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 917 AA; 101869 MW; 3DB304CE47EBEA7A CRC64;

Query Match 96.3%; Score 52; DB 2; Length 917;  
 Best Local Similarity 75.0%; Pred. No. 0.15;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2 TFCGTXXXAPE 13
DB      |||||
        674 TFCGTEYLAPE 685

RESULT 37
ID Q5B5E2 EMENI PRELIMINARY; PRT; 919 AA.
AC Q5B5E2
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=AN4238.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre B., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Katatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Menga V., Murphy T., Naylor J., Nguyen C., Nicol D.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramaeamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Genome sequence of Aspergillus nidulans";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AACD0100068; EAA59337.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 919 AA; 101446 MW; B459EEA4173E78E2 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 919;
Best Local Similarity 75.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXXAPE 13
DB      |||||
        683 TFCGTEYLAPE 694

RESULT 38
ID Q8N1K8 EMENI PRELIMINARY; PRT; 919 AA.
AC Q8N1K8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE CAMP-dependent protein kinase-like.
GN Name=echa;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.

```

```

OX NCBI_TaxID=162425;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22040566; PubMed=12046590;
RA Filling S., Chaveroche M.K., Shimizu K., Keller N., d'Enfert C.;
RT "CAMP and ras signalling independently control spore germination in
RT the filamentous fungus Aspergillus nidulans.";
RL Mol. Microbiol. 44:1001-1016(2002).
DR EMBL: AY043352; AAK71879.1; -; Genomic_DNA.
DR HSSP; P31751; 1MRV.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004648; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR000961; Pkinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase C; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 919 AA; 101447 MW; B459EEA4173E78E2 CRC64;

Query Match 96.3%; Score 52; DB 2; Length 919;
Best Local Similarity 75.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXXAPE 13
DB      |||||
        683 TFCGTEYLAPE 694

RESULT 39
ID Q4P998 USTMA PRELIMINARY; PRT; 1210 AA.
AC Q4P998
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=UM03315.1;
OS Ustilago maydis 521.
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=237631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=521;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseis M., Karlsson E.,
RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,

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RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,  
RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,  
RA Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,  
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,  
RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mienga V., Moru K.,  
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,  
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,  
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pignani B.,  
RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond P.,  
RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,  
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,  
RA Spencer B., Staiker J., Stange-thomann N., Stavropoulos S.,  
RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,  
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,  
RA Towey S., Tsamla T., Taomo N., Vallee D., Vassiliev H.,  
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,  
RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
RA Zimmer A., Zody M., Lander E.;  
RT "The genome sequence of *Ustilago maydis*.";  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACPO1000112; EAK84302.1; -; Genomic\_DNA.  
KW Hypothetical protein.  
SQ SEQUENCE 1210AA; 131030 MW; B4A812F4430D21CC CRC64;

Query Match 96.3%; Score 52; DB 2; Length 1210;  
Best Local Similarity 75.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXYXAPE 13  
||||| |||||  
DB 635 TFCGTAEYLAPE 646

RESULT 40  
Q8NJW8 USTMA  
ID Q8NJW8 USTMA PRELIMINARY; PRT; 1216 AA.  
AC Q8NJW8  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Serine/threonine protein kinase B-related Ukb1.  
GN Name=ukb1;  
OS *Ustilago maydis* (Smut fungus).  
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; *Ustilago*.  
OX NCBI\_TaxID=5270;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=518;  
RX MEDLINE=22111628; PubMed=12231194; DOI=10.1016/S1087-1845(02)00030-0;  
RA Abramovitch R.B., Yang G., Kronstad J.W.;  
RT "The ukb1 gene encodes a putative protein kinase required for bud site  
RT selection and pathogenicity in *Ustilago maydis*.";  
RL Fungal Genet. Biol. 37:98-108(2002).  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
DR EMBL; AF487462; AAL93208.2; -; Genomic\_DNA.  
DR HSSP; F31751; IGZK.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF00433; Pkinase C; 1.  
DR ProDom; PD000001; Prot\_kinase; 2.

DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1216 AA; 131687 MW; 1BC98E037C90117C CRC64;  
Query Match 96.3%; Score 52; DB 2; Length 1216;  
Best Local Similarity 75.0%; Pred. No. 0.19;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXXYXAPE 13  
||||| |||||  
DB 635 TFCGTAEYLAPE 646  
Search completed: February 18, 2006, 08:01:02  
Job time : 203.053 secs



GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM protein - protein search, using sw model  
 Run on: February 18, 2006, 07:50:48 ; Search time 203.211 Seconds  
 (without alignments)  
 28.108 Million cell updates/sec

Title: US-09-868-131C-48  
 Perfect score: 54 ;  
 Sequence: 1 XTCGTXVXKPE 13

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq\_21.\*

1: Geneseqp1980s.\*  
 2: Geneseqp1990s.\*  
 3: Geneseqp2000s.\*  
 4: Geneseqp2001s.\*  
 5: Geneseqp2002s.\*  
 6: Geneseqp2003as.\*  
 7: Geneseqp2003bs.\*  
 8: Geneseqp2004s.\*  
 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	96.3	375	7 ABU61669	Abu61669 Yeast Sch
2	52	96.3	494	8 ADN23646	Adn23646 Bacterial
3	52	96.3	554	8 ADN20437	Adn20437 Bacterial
4	52	96.3	581	8 ADN23422	Adn23422 Bacterial
5	52	96.3	646	8 ADN19627	Adn19627 Bacterial
6	52	96.3	699	3 AAB03445	Aab03445 Candida
7	52	96.3	699	5 ABP73798	Abp73798 Candida
8	52	96.3	768	8 ADN19561	Adn19561 Bacterial
9	52	96.3	776	2 AAW73894	Aaw73894 Yeast MEC
10	52	96.3	821	2 AAW26664	Aaw26664 Yeast che
11	52	96.3	821	5 ABP54942	Abp54942 Saccharom
12	52	96.3	821	6 ABR53872	Abr53872 Protein s
13	52	96.3	821	7 ABU61612	Abu61612 Yeast SPK
14	52	96.3	821	7 ADK64880	Adk64880 Disease t
15	52	96.3	821	9 ADY86780	Ady86780 Yeast SPK
16	52	96.3	821	9 AEA89422	Aea89422 Yeast SPK
17	52	96.3	823	8 ADS43637	Ads43637 Bacterial
18	51	94.4	12	8 ADJ38835	Adj38835 p70-S6k-a
19	51	94.4	12	8 ADJ38836	Adj38836 p70-S6k-b
20	51	94.4	13	3 AAY95274	Aay95274 Serum and
21	51	94.4	13	3 AAY93507	Aay93507 Consensus
22	51	94.4	17	3 AAY93528	Aay93528 p70S6k-al
23	51	94.4	198	4 AAU11803	Aau11803 Human par
24	51	94.4	258	5 AAE23310	Aae23310 Human p54

25	51	94.4	268	5	AAE23316	Aae23316 Human p85
26	51	94.4	281	4	AAQ67390	Aaq67390 Partial a
27	51	94.4	296	8	ADI40838	Adi40838 Human kin
28	51	94.4	311	8	ADN21222	Adn21222 Bacterial
29	51	94.4	318	4	AAB99825	Aab99825 AGC prote
30	51	94.4	318	4	AAB99824	Aab99824 AGC prote
31	51	94.4	318	8	ADJ38873	Adj38873 p70S6Kbet
32	51	94.4	318	8	ADJ38872	Adj38872 p70S6Kalp
33	51	94.4	333	6	ABR57464	Abr57464 AGC famil
34	51	94.4	338	3	AAY77845	Aay77845 Human ser
35	51	94.4	342	8	ADX91853	Adx91853 Plant ful
36	51	94.4	372	8	ADP29809	Adp29809 Human sec
37	51	94.4	403	8	ADX74016	Adx74016 Plant ful
38	51	94.4	427	8	ADX73686	Adx73686 Plant ful
39	51	94.4	439	8	ADX71518	Adx71518 Plant ful
40	51	94.4	445	8	ADU66586	Adu66586 Human kin
41	51	94.4	446	8	ABM83991	Abm83991 Human dia
42	51	94.4	464	8	ADS23961	Ads23961 Bacterial
43	51	94.4	469	8	ADX95105	Adx95105 Plant ful
44	51	94.4	471	4	AAB99817	Aab99817 AGC prote
45	51	94.4	477	7	ADL18513	Adl18513 Maize rec
46	51	94.4	482	5	AAE233306	Aae233306 Human p54
47	51	94.4	482	5	AAE233321	Aae233321 Human p85
48	51	94.4	482	5	AAE233320	Aae233320 Human p54
49	51	94.4	483	8	ADU20436	Adu20436 A. thalia
50	51	94.4	483	8	ADU20583	Adu20583 A. thalia
51	51	94.4	490	4	ABE65097	Abbe65097 Drosophil
52	51	94.4	495	3	AAAY45007	Aay45007 p70 (beta
53	51	94.4	495	5	AAE233307	Aae233307 Human p85
54	51	94.4	495	8	ADU18029	Adu18029 Human can
55	51	94.4	495	9	ADX07940	Adx07940 Cyclin-de
56	51	94.4	502	7	ADE83374	Ade83374 Human Pro
57	51	94.4	502	7	ADE57839	Ade57839 Rat Prote
58	51	94.4	502	7	ADE57841	Ade57841 Human Pro
59	51	94.4	502	7	ADE83372	Ade83372 Rat Prote
60	51	94.4	502	7	ADF30469	Adf30469 Rat angio
61	51	94.4	502	8	ADF43132	Adf43132 Human p70
62	51	94.4	502	8	ADX91396	Adx91396 Plant ful
63	51	94.4	525	6	ABP97365	Abp97365 Human p70
64	51	94.4	525	7	ADF30471	Adf30471 Rat angio
65	51	94.4	525	8	ADT60495	Adt60495 Plant pol
66	51	94.4	541	8	ADX74412	Adx74412 Plant ful
67	51	94.4	554	8	ADX90099	Adx90099 Plant ful
68	51	94.4	609	8	ADS44244	Ads44244 Bacterial
69	51	94.4	637	2	AAW522394	Aaw522394 Drosophil
70	51	94.4	707	8	ADM41439	Adm41439 Caenorhab
71	50	92.6	12	8	ADJ38825	Adj38825 SGK3 acti
72	50	92.6	12	8	ADJ38829	Adj38829 PKC-gamma
73	50	92.6	12	8	ADJ38817	Adj38817 PKB-gamma
74	50	92.6	12	8	ADJ38832	Adj38832 PKC-lota
75	50	92.6	12	8	ADJ38831	Adj38831 PKC-zeta
76	50	92.6	12	8	ADJ38827	Adj38827 PKC-beta-
77	50	92.6	12	8	ADJ38830	Adj38830 PKC-delta
78	50	92.6	12	8	ADJ38824	Adj38824 SGK2 acti
79	50	92.6	12	8	ADJ38818	Adj38818 SGK1 acti
80	50	92.6	12	8	ADJ38816	Adj38816 PKB-beta
81	50	92.6	12	8	ADJ38815	Adj38815 PKB-alpha
82	50	92.6	12	8	ADJ38826	Adj38826 PKC-beta-
83	50	92.6	12	8	ADJ38828	Adj38828 PKC-beta-
84	50	92.6	12	8	ADQ76099	Adq76099 Peptide o
85	50	92.6	12	8	ADQ76101	Adq76101 Peptide o
86	50	92.6	12	8	ADQ76105	Adq76105 Peptide o
87	50	92.6	12	8	ADQ76102	Adq76102 Peptide o
88	50	92.6	12	8	ADM24783	Adm24783 PDK1 MEKK
89	50	92.6	16	4	AAB999811	Aab999811 PDK1 pept
90	50	92.6	16	4	AAB999795	Aab999795 3-phospho
91	50	92.6	16	3	ADJ38898	Adj38898 Synthetic
92	50	92.6	17	3	AAY93529	Aay93529 PKC seque
93	50	92.6	17	3	AAY93527	Aay93527 PKB-alpha
94	50	92.6	17	3	ADY20890	Ady20890 Activatio
95	50	92.6	19	9	ADY20889	Ady20889 Activatio
96	50	92.6	19	9	ADY20889	Ady20889 Activatio
97	50	92.6	20	9	AEB24422	Aeb24422 Protein k

98 50 92.6 28 9 ADW81261 Adw81261 AMPK modu  
99 50 92.6 35 5 AAE22774 Aae22774 Human SGK  
100 50 92.6 36 3 AAB13221 Aab13221 AKT/akt-1

ALIGNMENTS

RESULT 1  
ABU61669  
ID ABU61669 standard; protein; 375 AA.  
XX  
AC ABU61669;  
XX  
DT 15-AUG-2003 (first entry)  
XX  
DE Yeast Sch9 serine/threonine kinase putative catalytic domain.  
XX  
KW Eukaryote; yeast; Sch9; serine/threonine kinase; enzyme;  
KW catalytic domain; aging-dependent disease; long-lived yeast mutant;  
KW toxicity; antiaging.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN US2003044946-A1.  
XX  
PD 06-MAR-2003.  
XX  
PF 03-APR-2002; 2002US-00116722.  
XX  
PR 03-APR-2001; 2001US-0281213P.  
XX  
PA (LONG/) LONGO V.D.  
XX  
PI Longo VD;  
XX  
DR WPI; 2003-456559/43.  
XX  
PT New agents which extend the lifespan of eukaryotes and modulates a  
PT pathway, useful for extending the longevity of and preventing or treating  
PT aging-dependent diseases in eukaryote.  
XX  
PS Disclosure; Fig 5; 31pp; English.  
XX  
CC The invention relates to an agent for extending the lifespan of a  
CC eukaryote which modulates a pathway. The invention also relates to a  
CC method for increasing the lifespan of a eukaryote comprising contacting  
CC the eukaryotic cell with an agent above and a system for studying the  
CC aging and death of a eukaryote comprising a long-lived yeast mutant. The  
CC agent is useful for extending the lifespan of a eukaryote, specifically  
CC for extending the longevity of and preventing or treating aging-dependent  
CC diseases in a eukaryote. The long lived-mutants can be used to identify  
CC drugs that prevent the toxicity of specific toxins or mutagens, and to  
CC screen for drugs that affect the function of human proteins inserted into  
CC yeast cells lacking the yeast homologue of that particular human protein  
CC but do not decrease long term survival. This sequence represents the  
CC yeast Sch9 serine/threonine kinase putative catalytic domain. Yeast Sch9  
CC serine/threonine kinase genes are used as agents for modulating pathways  
CC in the scope of the invention  
XX  
SQ Sequence 375 AA;

Query Match 96.3%; Score 52; DB 7; Length 375;  
Best Local Similarity 75.0%; Pred. No. 0.37;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXXAPE 13  
||| |  
Db 208 TFCGTYEYLAPE 219

RESULT 2  
ADS23646

ID ADS23646 standard; protein; 494 AA.  
XX  
AC ADS23646;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #12679.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; oomosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR WPI; 2004-061375/06.  
XX  
PT New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 12679; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 494 AA;

Query Match 96.3%; Score 52; DB 8; Length 494;  
Best Local Similarity 75.0%; Pred. No. 0.48;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
Db 318 TFCGTTEYLAPE 329

RESULT 3  
ID ADN20437 standard; protein; 554 AA.  
AC ADN20437;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #3090.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR WPI; 2004-061375/06.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of photosynthesis or by  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 554 AA;  
SQ Query Match 96.3%; Score 52; DB 8; Length 554;  
Best Local Similarity 75.0%; Pred. No. 0.53;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
Db 367 TFCGTTEYLAPE 378

RESULT 4  
ID ADN23422 standard; protein; 581 AA.  
XX  
AC ADN23422;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Bacterial polypeptide #6075.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.  
XX  
OS Bacteria.  
XX  
PN US2003233675-A1.  
XX  
PD 18-DEC-2003.  
XX  
PF 20-FEB-2003; 2003US-00369493.  
XX  
PR 21-FEB-2002; 2002US-0360039P.  
XX  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
DR WPI; 2004-061375/06.  
XX  
CC New recombinant DNA construct comprising a promoter positioned to provide  
CC for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source, useful for producing plants with improved properties.  
XX  
PS Claim 1; SEQ ID NO 6075; 122pp; English.  
XX  
CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 581 AA;

Query Match 96.3%; Score 52; DB 8; Length 581;

Best Local Similarity 75.0%; Pred. No. 0.56;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13

||||| |||

Db 429 TFCGTAEYVAPE 440

RESULT 5

ADN19627

ID ADN19627 standard; protein; 646 AA.

AC ADN19627;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #2280.

XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.

PS Claim 1; SEQ ID NO 2280; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 646 AA;

Query Match 96.3%; Score 52; DB 8; Length 646;

Best Local Similarity 75.0%; Pred. No. 0.62;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13

||||| |||

Db 426 TFCGTTDYLAPE 437

RESULT 6

AAB03445

ID AAB03445 standard; protein; 699 AA.

XX AAB03445;

XX 03-JAN-2001 (first entry)

DE Candida albicans essential growth protein #3.

XX Growth inhibition; survival; pathogen; fungal infection; vulvovaginitis.

XX Candida albicans.

XX WO200034481-A2.

XX 15-JUN-2000.

XX 06-DEC-1999; 99WO-EP009833.

XX 04-DEC-1998; 98EP-00204122.

XX (JANC ) JANSSEN PHARM NV.

XX Contreras RH, Nelissen B, De Backer MD, Luyten WHML, Viaene JE;

XX Logghe MG, Vialard JE;

XX WPI; 2000-431302/37.

XX N-PSDB; AAA52791.

XX Novel nucleic acid molecule and polypeptides essential for survival and  
 PT growth of yeast candida albicans useful for treating candida albicans  
 PT associated diseases and for identifying antifungal compounds.

PS Claim 11; Fig 16; 112pp; English.

XX The present sequence is a protein which is essential for the survival and  
 CC growth of Candida albicans. This fungus causes infection, such as  
 CC vulvovaginitis, in humans, particularly in those who are  
 CC immunocompromised. The protein and its gene can be used to diagnose  
 CC infection, and they can be used as targets for inhibiting the  
 CC proliferation of the fungus. This protein and gene are particularly  
 CC useful as they are thought to be species-specific

XX Sequence 699 AA;

Query Match 96.3%; Score 52; DB 3; Length 699;

Best Local Similarity 75.0%; Pred. No. 0.66; Mismatches 0; Conservative 0; Indels 3; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| |

Db 331 TFCGTLAYVAPE 342

RESULT 7

ID ABP73798 standard; protein; 699 AA.

XX ABP73798;

DT 30-JAN-2003 (first entry)

XX Candida albicans essential protein SEQ ID NO 7635.

XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;

KW signal transduction; DNA replication; cell division; growth;

KW proliferation; Candida albicans; fungicide; antifungal.

XX Candida albicans.

XX WO200253728-A2.

XX 11-JUL-2002.

XX 26-DEC-2001; 2001WO-US049486.

XX 29-DEC-2000; 2000US-0259128P.

PR 20-FEB-2001; 2001US-00792024.

PR 22-AUG-2001; 2001US-0314050P.

XX (ELIT-) ELITRA PHARM INC.

XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

PI WPI; 2002-566694/60.

DR N-PSDB; AB232348.

XX Constructing strains for identifying gene products as effective targets

PT for therapeutic intervention, by inactivating in the strain one allele of

PT a gene and placing other allele of the gene under conditional expression.

XX Claim 44; SEQ ID NO 7635; 167pp + Sequence Listing; English.

XX The invention relates to constructing (M1) a strain of diploid fungal

CC cells in which both alleles of a gene are modified, comprising modifying

CC one allele by insertion or replacement by a cassette having an

CC expressible selectable marker and modifying other allele by

CC recombination, of a promoter replacement fragment with a heterologous

CC promoter, so that expression of the second allele is regulated by the

CC promoter. (M1) is useful for constructing a strain of diploid fungal

CC cells in which both alleles of a gene are modified. The diploid fungal

CC cells having both alleles modified are useful for identifying a gene that

CC is essential to the survival or growth of a fungus, a gene that

CC contributes to the virulence and/or pathogenicity of a fungus, a gene

CC that contributes to the resistance of a diploid fungus to an antifungal

CC agent, an antifungal agent that inhibits the growth of a diploid fungus

CC and for identifying a therapeutic agent for treatment of a mammalian

CC disease. (M1) is useful for identifying a compound which modulates the

CC activity of a gene product, preferably enzymatic activity, carbon

CC compound catabolism, biosynthetic, transporter, transcriptional,

CC translational, signal transduction, DNA replication and cell division

CC activity. The method is useful for identifying a compound having the

CC ability to inhibit growth or proliferation of C. albicans cells and for

CC treating infection by C. albicans. The present sequence is that of an

CC essential Candida albicans protein used in the method of the invention.

CC Note: The sequence data for this patent is not represented in the printed

CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office

XX

Seq Sequence 699 AA;

Query Match 96.3%; Score 52; DB 5; Length 699;

Best Local Similarity 75.0%; Pred. No. 0.66; Mismatches 0; Indels 3; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| |

Db 331 TFCGTLAYVAPE 342

RESULT 8

ID ADN19561 standard; protein; 768 AA.

XX ADN19561;

AC ADN19561;

XX 02-DEC-2004 (first entry)

DT Bacterial polypeptide #2214.

DE Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

PN 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 2214; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomanan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX  
 XX  
 SQ Sequence 768 AA;

Query Match 96.3%; Score 52; DB 8; Length 768;  
 Best Local Similarity 75.0%; Pred. No. 0.72;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 |||||  
 DB 517 TFCGTTTEYLAP 528

RESULT 9

AAW73894  
 ID AAW73894 standard; protein; 776 AA.

XX  
 AC AAW73894;

XX  
 DT 08-APR-1999 (first entry)

XX  
 DE Yeast MEC2 protein sequence.

XX  
 KW Cell cycle checkpoint gene; yeast; radiation resistance; detection;  
 KW G2/M checkpoint.

XX  
 OS Saccharomyces cerevisiae.

XX  
 PN US5866338-A.

XX  
 PD 02-FEB-1999.

XX  
 PF 06-JUN-1997; 97US-00870693.

XX  
 PR 12-MAY-1992; 92US-00882051.

XX  
 PR 14-MAY-1992; 92US-00884426.

XX  
 PR 12-MAY-1993; 93WO-US004458.

XX  
 PR 18-FEB-1994; 94US-00198446.

XX  
 (UNIW ) UNIV WASHINGTON.

PA (UYAR-) UNIV ARIZONA.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX  
 PI Plon SE, Groudine MT, Hartwell LH, Weinert TA;

XX  
 WPI; 1999-141919/12.

DR N-PSDB; AAX01275.

XX  
 PT Nucleotide sequences that hybridise to hRAD cDNA - method for isolating  
 PT human checkpoint cDNA, and antibody to CDC34.

XX  
 PS Example 4; Col 89-96; 73pp; English.

XX  
 CC This sequence is the yeast MEC2 protein. The DNA encoding this sequence  
 CC is necessary for G2/M cell cycle checkpoint control. This sequence was  
 CC identified using the method of the invention for isolating a human  
 CC checkpoint cDNA that is capable of restoring growth at a restrictive  
 CC temperature in a yeast test cell, where the yeast test cell comprises a  
 CC genome having a first gene that forms a DNA strand break at a restrictive  
 CC temperature and a second gene that fails to induce a cell cycle arrest in  
 CC response to the DNA strand break, whereby the growth of the yeast test  
 CC cell is inhibited at the restrictive temperature, comprising: (a)  
 CC obtaining a human cDNA library comprising several human cDNA clones; (b)  
 CC inserting the human cDNA clones individually into plasmid vectors  
 CC containing a selectable marker gene; (c) transforming a culture of the  
 CC yeast test cells with the plasmid vectors from the preceding step; (d)  
 CC selecting for yeast test cells transformed with the selectable marker  
 CC gene; (e) growing the selected transformants at the restrictive

CC temperature and isolating a candidate transformant capable of growing at  
 CC the restrictive temperature; and (f) identifying the human cDNA carried  
 CC by the candidate transformant as a human checkpoint cDNA by sequencing  
 CC the human cDNA carried by the candidate transformant and determining that  
 CC the human cDNA is less than 50% homologous with both the first gene and  
 CC the second gene. The nucleotide sequence of hRADcompB can be used to  
 CC confer radiation resistance on a cell

XX  
 SQ Sequence 776 AA;

Query Match 96.3%; Score 52; DB 2; Length 776;  
 Best Local Similarity 75.0%; Pred. No. 0.73;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 |||||  
 DB 354 TFCGTLAYVAPE 365

RESULT 10

AAW26664

ID AAW26664 standard; protein; 821 AA.

XX  
 AC AAW26664;

XX  
 DT 25-MAR-2003 (revised)

XX  
 DT 25-FEB-1998 (first entry)

XX  
 DE Yeast checkpoint control protein MEC2.

XX  
 KW MEC2; cell cycle; checkpoint gene; yeast; DNA damage; cancer; therapy.

XX  
 OS Saccharomyces cerevisiae.

XX  
 FH Key Location/Qualifiers

FT Protein 1..776

FT /note= "in the Sequence Listing MEC2 terminates at  
 FT residue 775"

XX  
 US5674996-A.

XX  
 PD 07-OCT-1997.

XX  
 PF 18-FEB-1994; 94US-00198446.

XX  
 PR 12-MAY-1992; 92US-00882051.

XX  
 PR 14-MAY-1992; 92US-00884426.

XX  
 PR 12-MAY-1993; 93WO-US004458.

XX  
 (UYAR-) UNIV ARIZONA.

PA (UNIW ) UNIV WASHINGTON.

PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.

XX  
 PI Groudine MT, Weinert TA, Plon SE, Hartwell LH;

XX  
 WPI; 1997-502392/46.

DR N-PSDB; AAT91040.

XX  
 PT Nucleotide sequence capable of hybridising with huCDC34 - which is human  
 PT checkpoint gene, useful to increase sensitivity of tumour cells to  
 PT chemotherapeutic drugs or radiation.

XX  
 PS Example 4; Col 85-90; 54pp; English.

XX  
 CC This protein is encoded by novel yeast checkpoint control gene MEC2 (see  
 CC AAT91040). Yeast checkpoint control genes RAD17, RAD24, MEC1, MEC2 and  
 CC MEC3 (AAT91037-41, respectively) are responsible for recognising if the  
 CC cell has suffered DNA damage in the form of radiation or chemical damage  
 CC or if the cell has failed to complete DNA replication because of chemical  
 CC inhibition or intrinsic error. Upon recognising damage or failure, the  
 CC genes are responsible for inhibiting mitosis. The purpose of this  
 CC checkpoint control is that it preserves the viability of the cell and the  
 CC integrity of the genome by providing the cell time to repair these

CC insults prior to undertaking mitosis. The genes are potentially useful in  
 CC developing cancer chemotherapeutics, cancer chemoprevention agents, and  
 CC environmental toxicology tests. They can be used to produce proteins (see  
 CC AAW26661-65) that can then be screened for chemical agents that would  
 CC interfere with checkpoint controls. Cloned genes can also be used to  
 CC develop yeast strains in which these genes are deleted. Such yeast  
 CC strains can then be used to find the homologous human genes (see AAT91034  
 CC -36). (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 XX

SQ Sequence 821 AA;

Query Match 96.3%; Score 52; DB 2; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |||||  
 Db 354 TFCGTLAYVAPE 365

RESULT 11

ABP54942  
 ID ABP54942 standard; peptide; 821 AA.

XX AC ABP54942;

XX DT 13-JAN-2003 (first entry)

XX DE Saccharomyces cerevisiae SPK1.

XX SPK1; tyrosine threonine kinase; TTK; protein kinase; enzyme;

KW mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;  
 KW gene therapy. ;

XX OS Saccharomyces cerevisiae.

XX PN WO200268444-A1.

XX PD 06-SEP-2002.

XX PF 21-FEB-2002; 2002WO-US005278.

XX PR 21-FEB-2001; 2001US-0271254P.

XX PA (CHIR ) CHIRON CORP.

XX PI Reinhard C, Jefferson AB, Chan VW;

XX PS WPI; 2002-698650/75.

XX DR N-PSDB; ABV73988.

XX Reducing growth of cancer cells comprises reducing Tyrosine Threonine  
 PT Kinase (TTK) activity, useful in diagnosing and treating disorders with  
 PT abnormal expression levels and activity of TTK, such as lung, colon,  
 PT prostate and ovarian cancer.

XX Disclosure; Page 77-78; 113pp; English.

XX The present sequence is the protein sequence of Saccharomyces cerevisiae  
 CC SPK1, a protein related to human tyrosine threonine kinase (TTK, see  
 CC ABP54938). TTK polynucleotides and polypeptides of the invention  
 CC encompass polynucleotides and polypeptides having sequence similarity or  
 CC sequence identity to human TTK and other genes and gene products related  
 CC to TTK, such as SPK1. The invention is based on the finding that TTK is  
 CC differentially expressed in various forms of cancer. It provides methods  
 CC for the identification of cancerous cells, especially breast cancer and  
 CC colon cancer cells, by detection of expression levels of TTK, as well as  
 CC diagnostic, prognostic and therapeutic methods. These methods can be used  
 CC as the basis of rational therapy. Assays for identifying molecules that  
 CC modulate the activity of these genes in cancers, as well as methods of  
 CC inhibiting tumour growth by inhibiting the activity of TTK are also  
 CC provided

XX

SQ Sequence 821 AA;

Query Match 96.3%; Score 52; DB 5; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |||||  
 Db 354 TFCGTLAYVAPE 365

RESULT 12

ABR53872

ID ABR53872 standard; protein; 821 AA.

XX AC ABR53872;

XX DT 20-JUN-2003 (first entry)

XX DE Protein sequence #SEQ ID 2609.

XX KW Multiprotein complex; eukaryote; drug target; diagnosis.

XX OS Saccharomyces cerevisiae.

XX PN EP1258494-A1.

XX PD 20-NOV-2002.

XX PF 20-DEC-2001; 2001EP-00130253.

XX PR 15-MAY-2001; 2001EP-00111774.

XX PA (CELL-) CELLZONE AG.

XX PI Bauer A, Gavin A, Grandi P, Krause R, Kruse UD, Kuester BD;

XX PI Marzioch M, Schultz JD, Superti-Furga GD;

XX DR WPI; 2003-250078/25.

XX DR N-PSDB; ACC61914.

XX New isolated protein complexes useful for diagnosing a disease or  
 PT disorder, or as a target for an active agent of a pharmaceutical,  
 PT preferably a drug target in the treatment or prevention of disease or  
 PT disorder.

XX Disclosure; SEQ ID NO 2609; 17pp + Sequence Listing; English.

XX The invention relates to multiprotein complexes from eukaryotes. Proteins  
 CC of the invention and DNA sequences encoding them are given in records  
 CC ABR52568-ABR53903 and ACC60610-ACC61944 respectively. The complexes are  
 CC obtainable by using a protein as a bait and isolating the set of proteins  
 CC which is attached thereto from cells. Such protein complexes may comprise  
 CC up to 30 distinct proteins. Protein complexes of the invention are useful  
 CC for diagnosing a disease or disorder, or as a target for an active agent  
 CC of a pharmaceutical, preferably a drug target in the treatment or  
 CC prevention of a disease or disorder. Note: The sequence data for this  
 CC patent is not represented in the printed specification, but is based on  
 CC sequence information supplied by the European Patent Office. The complete  
 CC document is available on CD-ROM

SQ Sequence 821 AA;

Query Match 96.3%; Score 52; DB 6; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |||||  
 Db 354 TFCGTLAYVAPE 365

RESULT 13

ABU61612  
ID ABU61612 standard; protein; 821 AA.  
XX AC ABU61612;  
XX DT 11-AUG-2003 (first entry)  
XX DE Yeast SPK1 protein.  
XX KW Yeast; tyrosine threonine kinase; TTK; cancer; cytostatic;  
KW mitotic checkpoint gene; SPK1.  
XX OS Saccharomyces cerevisiae.  
XX PN US2003045491-A1.  
XX PD 06-MAR-2003.  
XX PF 21-FEB-2002; 2002US-00081119.  
XX PR 23-FEB-2001; 2001US-0289813P.  
XX (REIN/) REINHARD C.  
PA (JEFF/) JEFFERSON A. B.  
PA (CHAN/) CHAN V. W.  
XX PI Reinhard C, Jefferson AB, Chan VW;  
XX WPI; 2003-456566/43.  
DR N-PSDB; ACA62264.  
XX  
PT Detecting cancer in a subject, by comparing expression levels of tyrosine  
PT threonine kinase polypeptide or polynucleotide in a subject cell and a  
PT normal cell, where an increase in the expression level in the test cell  
PT is indicative of cancer.  
XX  
PS Disclosure; Page 30-32; 79pp; English.  
XX  
CC The invention relates to detecting cancer (other than ovarian cancer) in  
CC a subject, comprising comparing the expression levels of tyrosine  
CC threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or  
CC polynucleotide in a test cell obtained from the subject and in a normal  
CC non-cancer cell, where an increase in the expression level of TTK protein  
CC or nucleic acid in the test cell compared to that in the normal cell,  
CC indicates the presence of cancer other than ovarian cancer. Also included  
CC are reducing growth of a cancerous cell (by contacting a cancerous cell  
CC with an amount of an agent effective to reduce TTK polypeptide activity  
CC in the cell), an assay for identifying a candidate agent that reduces  
CC growth of a cancerous cell (comprising: (i) detecting the activity of a  
CC TTK polypeptide in the presence of a candidate agent; and (ii) comparing  
CC the activity of TTK polypeptide in the presence of a candidate agent  
CC relative to TTK polypeptide activity in the absence of the candidate  
CC agent), identifying an agent that reduces TTK activity (comprising: (i)  
CC contacting a cancerous cell displaying elevated expression of a TTK-  
CC encoding polynucleotide with a candidate agent; and (ii) determining the  
CC effect of the candidate agent on TTK polypeptide activity) and assessing  
CC the prognosis of a cancerous disease other than ovarian cancer in a  
CC subject (comprising: (i) detecting expression of TTK -encoding  
CC polynucleotide in a test cancer cell of a subject; and (ii) comparing a  
CC level of expression of TTK-encoding polynucleotide in the test cancer  
CC cell with a level of expression of the polynucleotide in a control non-  
CC cancer cell, where the level of expression of TTK in the test cancer cell  
CC relative to the level of expression in the control non-cancer cell is  
CC indicative of the prognosis of the cancerous disease). The methods are  
CC useful for detecting cancer (other than ovarian cancer) in a subject,  
CC reducing growth of cancerous cells, identifying a candidate agent that  
CC reduces growth of a cancerous cell, identifying an agent that reduces TTK  
CC activity and assessing the prognosis of a cancerous disease other than  
CC ovarian cancer. The methods are also useful for determining the ability  
CC of a subject to respond to a particular therapy e.g. as a basis of  
CC rational therapy. The present sequence represents a closely related  
CC protein to human TTK, in this case yeast SPK1 (not defined)

SQ Sequence 821 AA;  
Query Match 96.3%; Score 52; DB 7; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.77;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXYXAPE 13  
Db 354 TFCGTLAYVAPE 365  
RESULT 14  
ADK64880  
ID ADK64880 standard; protein; 821 AA.  
XX AC ADK64880;  
XX DT 06-MAY-2004 (first entry)  
XX DE Disease treating protein complex-derived protein #1576.  
XX KW protein complex; drug target; diagnosis.  
XX OS Unidentified.  
XX PN EP1338608-A2.  
XX PD 27-AUG-2003.  
XX PF 20-DEC-2002; 2002EP-00102902.  
XX PR 20-DEC-2001; 2001EP-00130253.  
XX PA (CELL-) CELLZOME AG.  
XX PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;  
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;  
PI Michon A, Leutwein C, Rick J;  
XX WPI; 2003-638460/61.  
DR N-PSDB; ADK64881.  
XX  
PT New proteins and protein complexes from eukaryotes, useful as targets in  
PT drug screening, or in diagnosing or screening for the presence of a  
PT disease or disorder, or a predisposition for developing a disease or  
PT disorder in a subject.  
XX  
PS Disclosure; SEQ ID NO 3151; 13pp; English.  
XX  
CC The invention relates to novel protein complexes comprising a first and a  
CC second protein, or its derivative, fragment, homologue or variant. The  
CC proteins are selected from given protein complexes, which are not defined  
CC in the specification. The variants are encoded by nucleic acids that  
CC hybridize to the nucleic acids encoding the proteins under low stringency  
CC conditions. The protein complexes are useful as targets for an active  
CC agent of a pharmaceutical. These protein complexes are particularly  
CC useful as drugs targets for the treatment or preventing of a disease or  
CC disorder. The complexes and methods above are useful in diagnosing or  
CC screening for the presence of a disease or disorder or a predisposition  
CC for developing a disease or disorder in a subject. These are also useful  
CC in screening for a drug for treatment or prevention of a disease or  
CC disorder. The molecule that modulates the amount, activity or protein  
CC components of the complex is useful for the manufacture of a medicament  
CC for the treatment or prevention of a disease or disorder. This sequence  
CC corresponds to a protein of the invention. (Note: the sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained from the EPO in electronic format).  
XX  
SQ Sequence 821 AA;  
Query Match 96.3%; Score 52; DB 7; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.77;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



QY 2 TFCGTXYYXAPE 13  
 |||||  
 Db 354 TFCGTLAYVAPE 365

## RESULT 15

ADY86780  
 ID ADY86780 standard; protein; 821 AA.

XX AC ADY86780;

XX DT 02-JUN-2005 (first entry)

XX DE Yeast SPK1 protein, SEQ ID NO: 16.

XX KW Prognosis; cancer; cytostatic; neoplasm; tyrosine threonine kinase; TTK;  
 SPK1.

XX OS Saccharomyces cerevisiae.

XX PN US2005063974-A1.

XX PD 24-MAR-2005.

XX PF 27-SEP-2004; 2004US-00951477.

XX PR 21-FEB-2001; 2001US-0271354P.

XX PR 23-FEB-2001; 2001US-0289813P.

XX PR 21-FEB-2002; 2002US-00081119.

XX PA (REIN/) REINHARD C.

XX PA (JEFF/) JEFFERSON A B.

XX PA (CHAN/) CHAN V W.

XX PI Reinhard C, Jefferson AB, Chan VW;

XX DR WPI; 2005-241248/25.

XX DR N-PSDB; ADY86779.

XX PT Assessment of prognosis of a cancerous disease other than ovarian cancer  
 comprises detection and comparison of expression of a tyrosine threonine  
 kinase-encoding polynucleotide in a test cancer cell with a control non-  
 cancer cell.

XX PS Disclosure; SEQ ID NO 16; 78pp; English.

XX CC The invention relates to a method for assessing the prognosis of a  
 cancerous disease other than ovarian cancer which involves detection and  
 comparison of expression of a tyrosine threonine kinase (TTK)-encoding  
 polynucleotide in a test cancer cell with a control non-cancer cell. The  
 method is useful to assess the prognosis of a cancerous disease other  
 than ovarian cancer. It is useful to identify cancerous cells and to  
 determine the ability of a subject to respond to a particular therapy  
 e.g. as the basis of rational therapy. The present sequence is the TTK  
 related yeast SPK1 protein.

XX SQ Sequence 821 AA;

Query Match 96.3%; Score 52; DB 9; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
 |||||  
 Db 354 TFCGTLAYVAPE 365

## RESULT 16

AEA89422  
 ID AEA89422 standard; protein; 821 AA.

XX AC AEA89422;

XX DT 25-AUG-2005 (first entry)

XX DE Yeast SPK1 protein, SEQ ID NO: 16.

XX KW Drug screening; diagnosis; therapeutic; cancer; cytostatic; neoplasm;  
 SPK1.

XX OS Saccharomyces cerevisiae.

XX PN US2005130926-A1.

XX PD 16-JUN-2005.

XX PF 28-OCT-2004; 2004US-00977087.

XX PR 04-NOV-1998; 98US-0107112P.  
 06-JAN-1999; 99US-0114856P.  
 14-MAY-1999; 99US-0134112P.  
 26-JUL-1999; 99US-0145612P.  
 13-AUG-1999; 99US-0148936P.  
 03-NOV-1999; 99US-0043336P.  
 12-MAY-2000; 2000US-00570593.  
 25-JUL-2000; 2000US-00626301.  
 21-FEB-2001; 2001US-0271254P.  
 21-FEB-2002; 2002US-00081119.  
 06-FEB-2003; 2003US-00360848.  
 30-OCT-2003; 2003US-00698959.  
 22-JAN-2004; 2004US-00763692.

XX PA (CHIR ) CHIRON CORP.

XX PI Reinhard C, Jefferson AB, Chan VW, Kaufmann J, Xin H, Kennedy GC;  
 Harrowe G, Khoja H, Shyamala V;

XX DR WPI; 2005-457024/46.  
 DR N-PSDB; AEA89421.

XX PT New isolated human HX2004-6 polypeptide or isolated VSHK-1 polypeptide,  
 useful for diagnosing or treating cancer, where VSHK-1 is also used to  
 identify a VSHK-1 receptor ligand.

XX PS Disclosure; SEQ ID NO 16; 206pp; English.

XX CC The invention relates to human HX2004-6 protein and a seven transmembrane  
 receptor protein referred as VSHK-1 useful for diagnosing or treating  
 cancer. The invention also relates to a method for reducing the growth of  
 a cancerous cell. VSHK-1 is useful for identifying a VSHK-1 receptor  
 ligand and to identify a substance which modulates its signal  
 transduction activity. The HX2004-6 DNA is useful to detect the presence  
 of HX2004-6 in a biological sample (e.g. ductal epithelial cells from  
 tissue chosen from pancreas, colon and breast). The invention is useful  
 for screening drugs for the treatment of cancer. The present sequence is  
 the yeast SPK1 protein. This sequence is differentially expressed in  
 cancer cells.

XX SQ Sequence 821 AA;

Query Match 96.3%; Score 52; DB 9; Length 821;  
 Best Local Similarity 75.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
 |||||  
 Db 354 TFCGTLAYVAPE 365

RESULT 17  
 ADS43637  
 ID ADS43637 standard; protein; 823 AA.  
 XX AC ADS43637;  
 XX

DT 02-DEC-2004 (first entry)  
 XX Bacterial polypeptide #22067.  
 DE  
 XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.  
 XX  
 XX Bacteria.  
 XX  
 XX US2003233675-A1.  
 PN  
 XX 18-DEC-2003.  
 PD  
 XX 20-FEB-2003; 2003US-00369493.  
 PF  
 XX 21-FEB-2002; 2002US-0360039P.  
 PR  
 XX (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 XX  
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
 PI WPI; 2004-061375/06.  
 XX  
 XX New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.  
 PT  
 XX Claim 1; SEQ ID NO 22067; 122pp; English.  
 PS  
 XX The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transformed plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
 CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition. This sequence represents a bacterial polypeptide used in the  
 CC production of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 XX Sequence 823 AA;  
 SQ  
 Query Match 96.3%; Score 52; DB 8; Length 823;  
 Best Local Similarity 75.0%; Pred. No. 0.77;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXXAPE 13  
 |||||  
 DB 569 TFCGTTEYLAPE 580

RESULT 18  
 ADJ38835  
 ID ADJ38835 standard; peptide; 12 AA.  
 XX  
 AC ADJ38835;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE p70-S6K-alpha activation or T-loop peptide.  
 XX  
 KW phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;  
 KW protein kinase; catalytic domain; enzyme; hydrophobic pocket;  
 KW insulin signalling pathway; signalling; crystalline form;  
 KW protein co-ordinate data; three-dimensional structure; antifungal;  
 KW antidiabetic; cardiant; cytostatic; cerebroprotective; vasotrophic;  
 KW anorectic; protein kinase modulator; cancer; diabetes; obesity;  
 KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;  
 KW neural injury.  
 XX  
 OS Synthetic.  
 XX  
 XX WO2003104481-A2.  
 PN  
 XX 18-DEC-2003.  
 PD  
 XX 09-JUN-2003; 2003WO-GB002509.  
 PF  
 XX 08-JUN-2002; 2002GB-00013186.  
 PR  
 XX (UYDU-) UNIV DUNDEE.  
 PA  
 XX Alessi D, Blondi R, Komander D, Van AD;  
 PI WPI; 2004-062373/06.  
 XX  
 XX Selecting/designing compound for modulating activity of phosphoinositide  
 PT dependent protein kinase 1 by using molecular modelling to select/design  
 PT compound predicted to interact with protein kinase catalytic domain.  
 PT  
 XX Disclosure; Page 17; 383pp; English.  
 PS  
 XX The present invention describes a method (M1) for selecting or designing  
 CC a compound for modulating the activity of phosphoinositide dependent  
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to  
 CC select or design a compound that is predicted to interact with the  
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is  
 CC predicted to interact with the protein kinase catalytic domain. Also  
 CC described: (1) selecting or designing (M2) a compound for modulating the  
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein  
 CC kinase having a hydrophobic pocket in the position equivalent to the  
 CC hydrophobic pocket of human PDK1 that is defined by residues including  
 CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human  
 CC PDK1 and further having a phosphate binding pocket in the position  
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined  
 CC by residues including Lys76, Arg131, Thr148 and/or Glu150; (2) assessing  
 CC (M3) the activation state of a structure for a protein kinase; (3) a  
 CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a  
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that  
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);  
 CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1  
 CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein  
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a  
 CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),  
 CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of  
 CC a medicament for the treatment of a patient in need of modulation of  
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or  
 CC PDK1/S6K kinase, for example insulin signalling pathway and/or  
 CC PDK1/PDK2/SGK/PRK2/p70 S6 kinase/PRK2/PKC signalling; and (11) a  
 CC crystalline form (VI) of polypeptide as defined in (M1). (I) has  
 CC antifungal, antidiabetic, cardiant, cytostatic, cerebroprotective,  
 CC vasotrophic and anorectic activities, and can be used as a modulator of  
 CC protein kinase. (V) is useful for modulating the ability of protein

CC kinase to phosphorylate different substrates, e.g., different naturally  
 CC occurring polypeptides, to different extents. (V) inhibits or increases  
 CC the activity of protein kinase. The protein structures e.g., the co-  
 CC ordinates as provided in the specification are useful for designing  
 CC reagent useful in drug designing assays or characterisation of protein  
 CC kinase activity or regulation. (V) capable of producing the activity of  
 CC PKC, e.g., PKC beta, PKR1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is  
 CC useful in treating cancer. (V) capable of increasing the activity of  
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity  
 CC or may be useful in inhibiting apoptosis, thus useful in treating  
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)  
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction  
 CC and neural injury. (V) is useful as an antifungal agent. The present  
 CC sequence is used in the exemplification of the present invention.

XX Sequence 12 AA;

Query Match 94.4%; Score 51; DB 8; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |  
 Db 1 TFCGTIEYMAPE 12

RESULT 19

ADJ38836  
 ID ADJ38836 standard; peptide; 12 AA.

AC ADJ38836;

DT 06-MAY-2004 (first entry)

DE p70-S6K-beta activation or T-loop peptide.

XX phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;  
 KW protein kinase; catalytic domain; enzyme; hydrophobic pocket;  
 KW insulin signalling pathway; signalling; crystalline form;  
 KW protein co-ordinate data; three-dimensional structure; antifungal;  
 KW antidiabetic; cardiant; cytostatic; cerebroprotective; vasotropic;  
 KW anorectic; protein kinase modulator; cancer; diabetes; obesity;  
 KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;  
 KW neural injury.

XX Synthetic.

OS WO2003104481-A2.

PN 18-DEC-2003.

PD 09-JUN-2003; 2003WO-GB002509.

PF 08-JUN-2002; 2002GB-00013186.

PR (UYDU-) UNIV DUNDEE.

PA Alessi D, Biondi R, Komander D, Van AD;

PI WPI; 2004-062373/06.

XX Selecting/designing compound for modulating activity of phosphoinositide  
 PT dependent protein kinase 1 by using molecular modelling to select/design  
 PT compound predicted to interact with protein kinase catalytic domain.

XX Disclosure; Page 17; 383pp; English.

XX The present invention describes a method (M1) for selecting or designing  
 CC a compound for modulating the activity of phosphoinositide dependent  
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to  
 CC select or design a compound that is predicted to interact with the  
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is  
 CC predicted to interact with the protein kinase catalytic domain. Also

CC described: (1) selecting or designing (M2) a compound for modulating the  
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein  
 CC kinase having a hydrophobic pocket in the position equivalent to the  
 CC hydrophobic pocket of human PDK1 that is defined by residues including  
 CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human  
 CC PDK1 and further having a phosphate binding pocket in the position  
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined  
 CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing  
 CC (M3) the activation state of a structure for a protein kinase; (3) a  
 CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a  
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that  
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);  
 CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1  
 CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein  
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a  
 CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),  
 CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of  
 CC a medicament for the treatment of a patient in need of modulation of  
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or  
 CC p70 S6 kinase, for example insulin signalling pathway and/or  
 CC PDK1/PRK2/SGK/PKB/p70 S6 kinase/PRK2/PKC signalling; and (11) a  
 CC crystalline form (VI) of polypeptide as defined in (M1). (I) has  
 CC antifungal, antidiabetic, cardiant, cytostatic, cerebroprotective,  
 CC vasotropic and anorectic activities, and can be used as a modulator of  
 CC protein kinase. (V) is useful for modulating the ability of protein  
 CC kinase to phosphorylate different substrates, e.g., different naturally  
 CC occurring polypeptides, to different extents. (V) inhibits or increases  
 CC the activity of protein kinase. The protein structures e.g., the co-  
 CC ordinates as provided in the specification are useful for designing  
 CC reagent useful in drug designing assays or characterisation of protein  
 CC kinase activity or regulation. (V) capable of producing the activity of  
 CC PKC, e.g., PKC beta, PKR1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is  
 CC useful in treating cancer. (V) capable of increasing the activity of  
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity  
 CC or may be useful in inhibiting apoptosis, thus useful in treating  
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)  
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction  
 CC and neural injury. (V) is useful as an antifungal agent. The present  
 CC sequence is used in the exemplification of the present invention.

XX Sequence 12 AA;

Query Match 94.4%; Score 51; DB 8; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |  
 Db 1 TFCGTIEYMAPE 12

RESULT 20

AA95274

ID AA95274 standard; peptide; 13 AA.

AC AA95274;

XX 12-SEP-2000 (first entry)

XX Serum and glucocorticoid-induced protein kinase consensus.

XX Serum and glucocorticoid-induced protein kinase; SGK; phosphorylation;  
 KW cancer; diabetes; ischaemia; therapy.

OS Mammalia.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "basic residue"

FT Misc-difference 7 /label= Pro, Ile

FT Misc-difference 8 /label= Asp, Glu

```

FT Misc-difference 10
FT /note= "Leu, Ile, Met"
XX PN WO200035946-A1.
XX PD
XX PD 22-JUN-2000.
XX PF 14-DEC-1999; 99WO-GB004232.
XX PR 14-DEC-1998; 98US-0112217P.
XX PR 19-AUG-1999; 99GB-00019676.
XX PA (UYDU-) UNIV DUNDEE.
XX
XX Cohen P, Kobayashi T, Deak M;
XX WPI; 2000-442364/38.
XX
XX Modulation of serum and glucocorticoid-induced protein kinase (SGK) by
PT phosphorylation with 3-phosphoinositide-dependent protein kinase-1 (PDK1)
PT or dephosphorylation, useful for treatment of cancer, diabetes and
PT ischemic diseases.
XX
XX Disclosure; Page 11; 127pp; English.
XX
XX The present sequence is that of a consensus peptide from serum and
CC glucocorticoid-induced protein kinase (SGK) proteins (see AAY95275-79).
CC SGK is activated by phosphorylation and deactivated by dephosphorylation.
CC The invention provides methods of activating SGK activity by
CC phosphorylation using 3-phosphoinositide-dependent protein kinase-1
CC (PDK1), and of reducing the activity of SGK by dephosphorylation. The
CC invention also provides a method of identifying a compound that modulates
CC the activity of SGK. Such compounds are useful for treating patients
CC requiring modulation of SGK, such as patients with cancer, diabetes or
CC ischaemic disease
XX
XX Sequence 13 AA;
SQ
Query Match 94.4%; Score 51; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
DB |||||
2 TFCGTXXYXAPE 13

RESULT 21
AAY93507
ID AAY93507 standard; peptide; 13 AA.
XX AC AAY93507;
XX
XX 25-SEP-2000 (first entry)
XX
XX Consensus sequence for phosphorylation by a protein kinase.
DE
XX Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FT FT Misc-difference 7
FT /label= Pro, Ile
FT FT Misc-difference 8
FT /label= Asp, Glu
FT FT Misc-difference 10
FT /label= Leu, Ile, Met
XX
XX WO200036135-A2.

```

```

XX PD 22-JUN-2000.
XX PF 14-DEC-1999; 99WO-GB004228.
XX PR 14-DEC-1998; 98US-0112114P.
XX PA (MEDI-) MEDICAL RES COUNCIL.
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX Thorner JW, Alessi DR, Torrance PD, Casamayor A;
XX WPI; 2000-442391/38.
XX
XX Screening method identifying compounds which modulate protein kinase
PT activity for use in treating fungal infections and cancer.
XX
XX Disclosure; Page 51; 155pp; English.
XX
XX The present sequence represents a sequence which is phosphorylated by a
CC protein kinase. The specification describes a screening method to
CC identify a compound which modulates the activity of protein kinases from
CC different sources, using host yeast cells. The method is used to identify
CC a compound which modulates (inhibits) the activity of a protein kinase.
CC Pkh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2, human serum and
CC glucocorticoid induced protein kinase (SGK) or protein kinase B-alpha
CC (PKBalpha). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used
CC to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKBalpha or
CC p70S6 kinase. Compounds identified by the methods are used to treat
CC fungal infections e.g. thrush, and to treat cancer. To treat cancer, the
CC compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds
CC which activate PKB or PDK1 can be used in the treatment of diabetes or
CC obesity, and compounds which inhibit a fungal functional homologue of
CC PDK1 (Pkh1 or Pkh2) or SGK (Ypk1 or Yrk2) can be used as an antifungal
CC agent to treat Candida infections, e.g. thrush
XX
XX Sequence 13 AA;
SQ
Query Match 94.4%; Score 51; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
DB |||||
2 TFCGTXXYXAPE 13

RESULT 22
AAY93528
ID AAY93528 standard; peptide; 17 AA.
XX AC AAY93528;
XX
XX 25-SEP-2000 (first entry)
XX
XX p70S6K-alpha sequence for phosphorylation by protein kinase PDK1.
DE
XX Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
KW human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW 3-phosphoinositide-dependent protein kinase-1; PDK1; fungal infection;
KW thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX
XX Homo sapiens.
OS
XX
XX WO200036135-A2.
XX
XX 22-JUN-2000.
XX
XX 14-DEC-1999; 99WO-GB004228.
XX PR 14-DEC-1998; 98US-0112114P.
XX
XX (MEDI-) MEDICAL RES COUNCIL.

```

PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Thorner JW, Alessi DR, Torrance PD, Casamayor A;  
 XX  
 DR WPI; 2000-442391/38.  
 XX  
 PT Screening method identifying compounds which modulate protein kinase  
 XX activity for use in treating fungal infections and cancer.  
 XX  
 XX Disclosure; Fig 6A; 155pp; English.  
 XX  
 CC The present sequence represents a sequence which is phosphorylated by  
 CC protein kinase PDK1. The specification describes a screening method to  
 CC identify a compound which modulates the activity of protein kinases from  
 CC different sources, using host yeast cells. The method is used to identify  
 CC a compound which modulates (inhibits) the activity of a protein kinase.  
 CC PKh1 or Pkh2 phosphorylate and activate Ypk1, Yrk2, human serum and  
 CC glucocorticoid induced protein kinase (SGK) or protein kinase B-alpha  
 CC (pKbalph). 3-phosphoinositide-dependent protein kinase-1 (PDK1) is used  
 CC to phosphorylate and activate Ypk1 and Yrk2 or SGK but not PKbalph or  
 CC p70S6 kinase. Compounds identified by the methods are used to treat  
 CC fungal infections e.g. thrush, and to treat cancer. To treat cancer, the  
 CC compounds inhibit PKB, PDK1 or the activation of PKB by PDK1. Compounds  
 CC which activate PKB or PDK1 can be used in the treatment of diabetes or  
 CC obesity, and compounds which inhibit a fungal functional homologue of  
 CC PDK1 (Pkh1 or Pkh2) or SGK (Ypk1 or Yrk2) can be used as an antifungal  
 CC agent to treat Candida infections, e.g. thrush  
 XX  
 SQ Sequence 17 AA;  
 Query Match 94.4%; Score 51; DB 3; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 0.032;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXXAPE 13  
 Db |||||  
 6 TFCGTIEYNAPE 17  
 RESULT 23  
 AAU11803  
 ID AAU11803 standard; protein; 198 AA.  
 AC  
 AC AAU11803;  
 XX  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX  
 XX Human partial protein kinase SGK351.  
 XX  
 XX Human; SGK351; protein kinase; cancers; immune-related disease;  
 KW cardiovascular disease; neuronal-associated disease; metabolic disorder;  
 KW tissue cancer; haematopoietic cancer; central nervous system disorder;  
 KW peripheral nervous system disorder; Alzheimer's disease;  
 KW Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;  
 KW viral infection; prion infection; bacterial infection; fungal infection;  
 KW ocular disease; migraine; pain; sexual dysfunction; mood disorder;  
 KW attention disorder; cognition disorder; hypotension; hypertension;  
 KW psychotic disorder; neurological disorder; dyskinesia; gene therapy;  
 KW metabolic disorder; organ transplant rejection; chromosome 17q22-25.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200177338-A2.  
 PN  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX  
 XX 10-APR-2001; 2001WO-US011675.  
 PF  
 XX  
 XX 10-APR-2000; 2000US-0195953P.  
 PR  
 XX 01-MAY-2000; 2000US-0201015P.  
 PR  
 XX 22-JUN-2000; 2000US-0213805P.  
 XX  
 XX (SUGB-) SUGEN INC.  
 PA

XX Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;  
 PI Caenepeel S;  
 XX  
 DR WPI; 2001-657173/75.  
 DR N-PSDB; AAS19264.  
 XX  
 PT Novel kinase polypeptides useful for identifying modulators of kinase  
 XX polypeptide that are used for inhibiting kinase activity for treating  
 PT cancers, Alzheimer's disease, Parkinson's disease, multiple sclerosis.  
 XX  
 XX Claim 7; Fig 2B; 167pp; English.  
 PS  
 XX The invention relates to an isolated, enriched, or purified kinase  
 CC polypeptide comprising a 1360 or 198 residue amino acid sequence, fully  
 CC defined in specification, or comprising a kinase except which lacks one  
 CC or more of N- or C-terminal domain, C-terminal catalytic domain, a  
 CC catalytic domain, a coiled-coil structure region, a proline-rich region,  
 CC a spacer region, or a C-terminal tail. Also include are the encoding  
 CC polynucleotides. The novel kinase is useful for identifying a substance  
 CC that modulates the activity of a kinase. The polynucleotide is useful for  
 CC detecting nucleic acid encoding a kinase. The polypeptide in a sample. The  
 CC kinases, polynucleotides modulators of the kinases and anti-kinase  
 CC antibodies are useful for diagnosing and treating a disease or disorder  
 CC such as cancers, immune-related disease and disorders, cardiovascular  
 CC disease, brain or neuronal-associated diseases, and metabolic disorders,  
 CC e.g. cancers of tissues, cancers of haematopoietic origin, diseases of  
 CC the central or peripheral nervous system, Alzheimer's disease,  
 CC Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis,  
 CC viral infections, infections caused by prions, infections caused by  
 CC bacteria, infections caused by fungi, or ocular diseases, migraine, pain,  
 CC sexual dysfunction, mood disorders, attention disorders, cognition  
 CC disorders, dyskinesias, metabolic disorders, or organ transplant  
 CC rejection and many other diseases and disorders given in the  
 CC specification. The polynucleotide is useful in gene therapy techniques.  
 CC The two novel kinases are designated SGK341 (the gene is located on  
 CC chromosome Xp22.1) and SGK351 (chromosome 17q22-25). The present sequence  
 CC is the novel kinase SGK351  
 XX  
 SQ Sequence 198 AA;  
 Query Match 94.4%; Score 51; DB 4; Length 198;  
 Best Local Similarity 75.0%; Pred. No. 0.31;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXXAPE 13  
 Db |||||  
 75 TFCGTIEYNAPE 86  
 RESULT 24  
 AA223310  
 ID AA223310 standard; protein; 258 AA.  
 XX  
 AC AA223310;  
 XX  
 XX 27-AUG-2002 (first entry)  
 DT  
 XX Human p54S6K protein catalytic domain.  
 DE  
 XX  
 XX Human; mammalian kinase; p54S6K; p85S6K; antibody generation; cancer;  
 KW diagnosis; drug identification; cytostatic; enzyme.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX US6372467-B1.  
 PN  
 XX  
 XX 16-APR-2002.  
 PD  
 XX  
 XX 29-OCT-1999; 99US-00430564.  
 PF  
 XX  
 XX 29-OCT-1998; 98US-0106141P.  
 PR

XX (HARD ) HARVARD COLLEGE.  
XX Blenis J, Lee-Fruman KK, Kuo CJ;  
XX WPI; 2002-424732/45.  
XX Isolated mammalian p54S6K and p85S6K kinases, useful for diagnosing and  
PT treating cancers.  
XX Disclosure; Col 29-30; 30pp; English.  
XX The invention relates to mammalian kinases, p54S6K and p85S6K and methods  
CC for identifying compounds that modulate, or which are modulated by p54S6K  
CC and p85S6K. The p54S6K and p85S6K kinases may be used as antigens to  
CC generate antibodies that may be used in immunoassays to detect and  
CC quantitate the presence of p54S6K and p85S6K kinases in samples and  
CC therefore be used to diagnose diseases, e.g. cancers. They may also be  
CC used in assays as drug targets to identify potential drugs for the  
CC treatment of diseases associated with p54S6K and p85S6K kinase expression  
CC and activity. The present sequence is human p54S6K protein catalytic  
CC domain  
XX  
SQ Sequence 258 AA;  
Query Match 94.4%; Score 51; DB 5; Length 258;  
Best Local Similarity 75.0%; Pred. NO. 0.4;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXYXAPE 13  
DB 164 TFCGTIEYMAPE 175  
RESULT 25  
AAE23316  
ID AAE23316 standard; peptide; 260 AA.  
XX  
AC AAE23316;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human p85S6K protein catalytic domain.  
XX  
KW Human; mammalian kinase; p54S6K; p85S6K; antibody generation; cancer;  
KW diagnosis; drug identification; cytostatic; enzyme.  
XX  
OS Homo sapiens.  
XX  
FN US6372467-B1.  
XX  
PD 16-APR-2002.  
XX  
PF 29-OCT-1999; 99US-00430564.  
XX  
PR 29-OCT-1998; 98US-0106141P.  
XX (HARD ) HARVARD COLLEGE.  
XX  
PI Blenis J, Lee-Fruman KK, Kuo CJ;  
XX  
DR WPI; 2002-424732/45.  
XX  
PT Isolated mammalian p54S6K and p85S6K kinases, useful for diagnosing and  
PT treating cancers.  
XX  
PS Disclosure; Col 33-34; 30pp; English.  
XX  
CC The invention relates to mammalian kinases, p54S6K and p85S6K and methods  
CC for identifying compounds that modulate, or which are modulated by p54S6K  
CC and p85S6K. The p54S6K and p85S6K kinases may be used as antigens to  
CC generate antibodies that may be used in immunoassays to detect and  
CC quantitate the presence of p54S6K and p85S6K kinases in samples and

CC therefore be used to diagnose diseases, e.g. cancers. They may also be  
CC used in assays as drug targets to identify potential drugs for the  
CC treatment of diseases associated with p54S6K and p85S6K kinase expression  
CC and activity. The present sequence is human p85S6K protein catalytic  
CC domain  
XX  
SQ Sequence 268 AA;  
Query Match 94.4%; Score 51; DB 5; Length 268;  
Best Local Similarity 75.0%; Pred. NO. 0.41;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXYXAPE 13  
DB 164 TFCGTIEYMAPE 175  
RESULT 26  
AAG67390  
ID AAG67390 standard; protein; 281 AA.  
XX  
AC AAG67390;  
XX  
DT 13-NOV-2001 (first entry)  
XX  
DE Partial amino acid sequence of human protein kinase SGK216.  
XX  
KW Human; protein kinase; cancer; immune disease; cardiovascular disease;  
KW brain disease; neuronal disease; Alzheimer's disease; chromosome 17;  
KW Parkinson's disease; multiple sclerosis; metabolic disorder;  
KW peripheral nervous system disease; amyotrophic lateral sclerosis;  
KW infection; ocular disease; migraine; pain; sexual dysfunction;  
KW mood disorder; attention disorder; cognition disorder; hypotension;  
KW hypertension; psychotic disorder; dyskinesia; transplant rejection.  
XX  
OS Homo sapiens.  
XX  
FN WO200166594-A2.  
XX  
PD 13-SEP-2001.  
XX  
PF 02-MAR-2001; 2001WO-US006838.  
XX  
PR 06-MAR-2000; 2000US-0187150P.  
PR 29-MAR-2000; 2000US-0193404P.  
PR 13-NOV-2000; 2000US-0247013P.  
XX (SUGE-) SUGEN INC.  
XX  
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
XX  
DR WPI; 2001-536777/59.  
XX N-PSDB; AAH77989.  
XX  
PT Nucleic acids capable of encoding human polypeptides having a kinase or  
PT kinase-like activity, useful for diagnosing a disease selected from  
PT cancers, cardiovascular disease and neuronal-associated diseases (e.g.  
PT Alzheimer's disease).  
XX  
PS Claim 7; Fig 2A; 201pp; English.  
XX  
CC The present sequence represents a partial human protein kinase. The gene  
CC is located at chromosomal position 17q21.2-Q22. The kinase polypeptides  
CC are useful for diagnosing a disease or disorder selected from cancers  
CC (e.g. cancers of tissues and cancers of hematopoietic origin), immune-  
CC related diseases and disorders, cardiovascular disease, brain or neuronal  
CC -associated diseases (e.g. Alzheimer's disease, Parkinson's disease,  
CC multiple sclerosis), metabolic disorders, peripheral nervous system  
CC diseases, amyotrophic lateral sclerosis, viral infections, infections  
CC caused by prions, infections caused by bacteria, infections caused by  
CC fungi, ocular diseases, migraines, pain, sexual dysfunction, mood  
CC disorders, attention disorders, cognition disorders, hypotension,  
CC hypertension, psychotic disorders, dyskinesias, and organ transplant

CC rejection. Kinase inhibitors are useful for treating diseases and  
 CC disorders described above

XX Sequence 281 AA;  
 SQ Query Match 94.4%; Score 51; DB 4; Length 281;  
 Best Local Similarity 75.0%; Pred. No. 0.43;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 ||||| |||||  
 Db 125 TFCGTIEYMAPE 136

## RESULT 27

ADI40838  
 ID ADI40838 standard; protein; 296 AA.

XX AC ADI40838;

DT 22-APR-2004 (first entry)

XX Human kinase and phosphatase KPP-4 protein SEQ ID NO:4.

DE human; kinase and phosphatase; KPP; enzyme; cardiovascular;  
 KW antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory;  
 KW antihypertensive; antiallergic; antidiabetic; nephrotropic; antitumor;  
 KW antihypertensive; antiallergic; antidiabetic; nephrotropic; antitumor;  
 KW gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic;  
 KW ophthalmological; antihypertensive; antiparkinsonian; neurotropic;  
 KW anticonvulsant; hepatotropic; CNS; antipsychotic; haemostatic;  
 KW cytotatic; antilipemic; antiparasitic; antihelminthic; antibacterial;  
 KW virucide; protozoicide; fungicide; Gene therapy; kinase modulator;  
 KW phosphatase modulator; cardiovascular disease; immune system disorder;  
 KW neurological disorder; growth and development disorder;  
 KW cell proliferative disorder; infection.

XX Homo sapiens.

XX WO2004009778-A2.

XX 29-JAN-2004.

XX 18-JUL-2003; 2003WO-US022650.

XX 19-JUL-2002; 2002US-0397354P.

PR 02-AUG-2002; 2002US-0400509P.

PR 02-AUG-2002; 2002US-0400783P.

PR 15-AUG-2002; 2002US-0404027P.

XX (INCY-) INCYTE CORP.

XX Hafalia AJA, Emerling BM, Kable AE, Richardson TW, Becha SD;  
 PI Baughn MR, Tang Y, Lal PG, Lee SY, Griffin JA, Khare R;  
 PI Elliott VS, Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tran UK;  
 PI Gururajan R, Ding L, Marquis JP, Thornton MB, Forsythe IJ, Lee EA;  
 PI Gietzen KJ, Ramkumar J;

XX WPI; 2004-132950/13.

DR N-PSDB; ADI40891.

XX New human kinases and phosphatases, useful for diagnosing, treating or  
 PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple  
 PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer  
 or hepatitis.

PS Claim 1; SEQ ID NO 4; 330pp; English.

XX The present sequence represents a human kinase and phosphatase (KPP)  
 CC protein. KPP sequences have cardiovascular, antiarteriosclerotic,  
 CC hypotensive, vasotropic, antiinflammatory, antihypertensive, anti-HIV,  
 CC antiallergic, antidiabetic, immunosuppressive, antihypertensive,  
 CC dermatological, antidiabetic, nephrotropic, antitumor, gastrointestinal,

CC neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological,  
 CC antirheumatic, antiparkinsonian, neurotropic, anticonvulsant, hepatotropic,  
 CC CNS, antipsychotic, haemostatic, cytotatic, antilipemic, antiparasitic,  
 CC antihelminthic, antibacterial, virucide, protozoicide and fungicide  
 CC activities, and can be used in gene therapy, and as kinase modulators and  
 CC phosphatase modulators. KPP proteins, polynucleotides, agonists and  
 CC antagonists can be used for diagnosing, treating or preventing disorders  
 CC associated with aberrant expression of KPP, such as cardiovascular  
 CC diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris  
 CC or congestive heart failure), immune system disorders (e.g. AIDS,  
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's  
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,  
 CC gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis,  
 CC osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,  
 CC Sjogren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's  
 CC disease, Parkinson's disease, Huntington's disease, dementia or  
 CC epilepsy), disorders affecting growth and development (e.g. cirrhosis,  
 CC hepatitis, mixed connective tissue disease, psoriasis or primary  
 CC thrombocytopenia), cell proliferative disorders (e.g.  
 CC hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial,  
 CC fungal, parasitic, protozoan or helminthic infections. The KPP and  
 CC polynucleotides are also useful in assessing the effects of exogenous  
 CC compounds on the expression of nucleic acids and kinases and  
 CC phosphatases, or for facilitating the drug discovery process, including  
 CC determination of efficacy, dosage, toxicity and pharmacology. The  
 CC polynucleotides encoding KPP are useful for creating transgenic animals  
 CC to model human disease.

XX SQ Sequence 296 AA;

Query Match 94.4%; Score 51; DB 8; Length 296;

Best Local Similarity 75.0%; Pred. No. 0.45;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13

||||| |||||

Db 228 TFCGTIEYMAPE 239

## RESULT 28

ADN21222

ID ADN21222 standard; protein; 311 AA.

XX AC ADN21222;

DT 02-DEC-2004 (first entry)

XX Bacterial polypeptide #3875.

XX Recombinant DNA construct; transformed plant; improved plant property;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KW pathogen tolerance; pest tolerance; plant disease resistance;  
 KW cell cycle pathway modification; plant growth regulator;  
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

XX (HINK/) HINKLE G J.

XX (SLAT/) SLATER S C.

XX (CHEN/) CHEN X.

XX (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a  
PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 3875; 122pp; English.  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactonan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at segdata.uspto.gov/sequence.html.  
XX  
XX Sequence 311 AA;

Query Match 94.4%; Score 51; DB 8; Length 311;  
Best Local Similarity 75.0%; Pred. No. 0.48;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 210 TFCGTCYSAPE 221

RESULT 29  
AAB99825  
ID AAB99825 standard; protein; 318 AA.

XX AAB99825;  
XX  
XX 20-SEP-2001 (first entry)  
XX  
XX AGC protein kinase family member p70S6Kbeta protein sequence.

XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;  
KW diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.  
XX  
XX Homo sapiens.  
OS Synthetic.

XX WO200144497-A2.  
XX  
XX 21-JUN-2001.

XX 04-DEC-2000; 2000WO-GB004598.  
XX  
XX 02-DEC-1999; 99US-0168559P.

XX (UYDU-) UNIV DUNDEE.  
XX  
XX Alessi D, Biondi R;

XX WPI; 2001-390252/41.  
XX  
XX Identifying modulators of protein kinase (PK) activity, useful in  
PT developing drugs for treating cancer or diabetes, by measuring the  
PT ability of the compound to modulate or mimic the interaction of PK with  
PT interacting polypeptides.  
XX  
XX Disclosure; Fig 16; 180pp; English.  
XX  
XX The present invention describes a method for identifying a compound that  
CC modulates protein kinase activity. The method comprises measuring the  
CC ability of the compound to inhibit, promote or mimic the interaction of a  
CC hydrophobic pocket-containing protein kinase with an interacting  
CC polypeptide. The interacting polypeptide interacts with the hydrophobic  
CC pocket of the protein kinase and/or comprises the amino acid sequence  
CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays for  
CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or  
CC polynucleotides from the present invention are useful in medicine, and  
CC particularly in the manufacture of a medicament for treating a patient in  
CC need of modulation of signalling by a hydrophobic pocket-containing  
CC protein kinase. Specifically, the patient has cancer or diabetes or is in  
CC need of inhibition of apoptosis, e.g. a patient suffering from tissue  
CC injury or ischaemic injury, including stroke. The compound or composition  
CC is also useful for inhibiting the degree or rate of phosphorylation by  
CC the protein kinase. The interacting polypeptide or compound is useful in  
CC methods of stabilising a hydrophobic pocket- containing protein kinase,  
CC where the protein kinase is exposed to the compound or polypeptide.  
CC AAB99786 to AAB99847 represent amino acid sequences, and AAH44210 and  
CC AAH44211 represent oligonucleotide sequences, used in the exemplification  
CC of the present invention

XX Sequence 318 AA;

Query Match 94.4%; Score 51; DB 4; Length 318;  
Best Local Similarity 75.0%; Pred. No. 0.49;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 149 TFCGTIEYMAPE 160

RESULT 30  
AAB99824  
ID AAB99824 standard; protein; 318 AA.

XX AAB99824;  
XX  
XX 20-SEP-2001 (first entry)  
XX  
XX AGC protein kinase family member p70S6Kalpha protein sequence.

XX Protein kinase; identification; hydrophobic pocket; interacting; cancer;  
KW diabetes; inhibition; apoptosis; tissue injury; ischaemic injury; stroke.  
XX  
XX Homo sapiens.  
OS Synthetic.

XX WO200144497-A2.  
XX  
XX 21-JUN-2001.

XX 04-DEC-2000; 2000WO-GB004598.  
XX  
XX 02-DEC-1999; 99US-0168559P.

XX (UYDU-) UNIV DUNDEE.  
XX  
XX Alessi D, Biondi R;

XX WPI; 2001-390252/41.  
XX



PT Identifying modulators of protein kinase (PK) activity, useful in  
 PT developing drugs for treating cancer or diabetes, by measuring the  
 PT ability of the compound to modulate or mimic the interaction of PK with  
 PT interacting polypeptides.

XX Disclosure; Fig 16; 180pp; English.

XX The present invention describes a method for identifying a compound that  
 CC modulates protein kinase activity. The method comprises measuring the  
 CC ability of the compound to inhibit, promote or mimic the interaction of a  
 CC hydrophobic pocket-containing protein kinase with an interacting  
 CC polypeptide. The interacting polypeptide interacts with the hydrophobic  
 CC pocket of the protein kinase and/or comprises the amino acid sequence  
 CC Phe/Tyr-Xaa-Xaa-Phe/Tyr (I). The method is useful in screening assays for  
 CC developing pharmaceutical compounds or drugs. Compounds, polypeptides or  
 CC polynucleotides from the present invention are useful in medicine,  
 CC particularly in the manufacture of a medicament for treating a patient in  
 CC need of modulation of signalling by a hydrophobic pocket-containing  
 CC protein kinase. Specifically, the patient has cancer or diabetes or is in  
 CC need of inhibition of apoptosis, e.g. a patient suffering from tissue  
 CC injury or ischaemic injury, including stroke. The compound or composition  
 CC is also useful for inhibiting the degree or rate of phosphorylation by  
 CC the protein kinase. The interacting polypeptide or compound is useful in  
 CC methods of stabilising a hydrophobic pocket- containing protein kinase,  
 CC where the protein kinase is exposed to the compound or polypeptide.  
 CC AAB95786 to AAB99847 represent amino acid sequences, and AAH44210 and  
 CC AAH44211 represent oligonucleotide sequences, used in the exemplification  
 CC of the present invention

XX Sequence 318 AA;

Query Match 94.4%; Score 51; DB 4; Length 318;  
 Best Local Similarity 75.0%; Pred. No. 0.49;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
 DB 149 TFCGTIETVNAPE 160

RESULT 31

ADJ38873  
 ID ADJ38873 standard; protein; 318 AA.

XX AC ADJ38873;

XX 06-MAY-2004 (first entry)

XX p70S6Kbeta amino acid sequence.

XX phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;  
 KW protein kinase; catalytic domain; enzyme; hydrophobic pocket;  
 KW insulin signalling pathway; signalling; crystalline form;  
 KW protein co-ordinate data; three-dimensional structure; antifungal;  
 KW antidiabetic; cardiant; cytostatic; cerebroprotective; vasotropic;  
 KW anorectic; protein kinase modulator; cancer; diabetes; obesity;  
 KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;  
 KW neural injury.

OS Unidentified.

XX W02003104481-A2.

XX 18-DEC-2003.

XX 09-JUN-2003; 2003WO-GB002509.

XX 08-JUN-2002; 2002GB-00013186.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Biondi R, Komander D, Van AD;

DR WPI; 2004-062373/06.

XX Selecting/designing compound for modulating activity of phosphoinositide  
 PT dependent protein kinase 1 by using molecular modelling to select/design  
 PT compound predicted to interact with protein kinase catalytic domain.

XX Disclosure; Fig 7; 383pp; English.

XX The present invention describes a method (M1) for selecting or designing  
 CC a compound for modulating the activity of phosphoinositide dependent  
 CC protein kinase 1 (PDK1) comprising using molecular modelling means to  
 CC select or design a compound that is predicted to interact with the  
 CC protein kinase catalytic domain of PDK1, and selecting a compound that is  
 CC predicted to interact with the protein kinase catalytic domain. Also  
 CC described: (1) selecting or designing (M2) a compound for modulating the  
 CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein  
 CC kinase having a hydrophobic pocket in the position equivalent to the  
 CC hydrophobic pocket of human PDK1 that is defined by residues including  
 CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human  
 CC PDK1 and further having a phosphate binding pocket in the position  
 CC equivalent to the phosphate binding pocket of human PDK1 that is defined  
 CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing  
 CC (M3) the activation state of a structure for a protein kinase; (3) a  
 CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a  
 CC host cell (III) comprising (II); (6) identifying (M4) a compound that  
 CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);  
 CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1  
 CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein  
 CC kinase mutated at the phosphate binding site, or vice versa; (8) a  
 CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),  
 CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of  
 CC a medicament for the treatment of a patient in need of modulation of  
 CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or  
 CC PDK1/PDK2/SGK/PKB/p70 S6 kinase/PRK2/PKC signalling; and (11) a  
 CC crystalline form (VI) of polypeptide as defined in (M1). (I) has  
 CC antifungal, antidiabetic, cardiant, cytostatic, cerebroprotective,  
 CC vasotropic and anorectic activities, and can be used as a modulator of  
 CC protein kinase. (V) is useful for modulating the ability of protein  
 CC kinase to phosphorylate different substrates, e.g., different naturally  
 CC occurring polypeptides, to different extents. (V) inhibits or increases  
 CC the activity of protein kinase. The protein structures e.g., the co-  
 CC ordinates as provided in the specification are useful for designing  
 CC reagent useful in drug designing assays or characterisation of protein  
 CC kinase activity or regulation. (V) capable of producing the activity of  
 CC PKC, e.g., PKC beta, PRK1 or PRK2, PDK1, PKB, SGK or p70 S6 kinase, is  
 CC useful in treating cancer. (V) capable of increasing the activity of  
 CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity  
 CC or may be useful in inhibiting apoptosis, thus useful in treating  
 CC diseases in which apoptosis is involved e.g., mechanical (including heat)  
 CC tissue injury or ischaemia disease such as stroke, myocardial infarction  
 CC and neural injury. (V) is useful as an antifungal agent. The present  
 CC sequence is used in the exemplification of the present invention.

XX Sequence 318 AA;

Query Match 94.4%; Score 51; DB 8; Length 318;  
 Best Local Similarity 75.0%; Pred. No. 0.49;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXAPE 13  
 DB 149 TFCGTIETVNAPE 160

RESULT 32

ADJ38872  
 ID ADJ38872 standard; protein; 318 AA.

XX AC ADJ38872;

XX 06-MAY-2004 (first entry)

DE p70S6Kalpha amino acid sequence.

XX phosphoinositide dependent protein kinase 1; PDK1; molecular modelling;

KW protein kinase; catalytic domain; enzyme; hydrophobic pocket;

KW insulin signalling pathway; signalling; crystalline form;

KW protein co-ordinate data; three-dimensional structure; antifungal;

KW antidiabetic; cardiant; cytostatic; cerebroprotective; vasotropic;

KW anorectic; protein kinase modulator; cancer; diabetes; obesity;

KW apoptosis inhibition; ischaemia disease; stroke; myocardial infarction;

KW neural injury.

XX Unidentified.

XX WO2003104481-A2.

PN 18-DEC-2003.

XX 09-JUN-2003; 2003WO-GB002509.

XX 08-JUN-2002; 2002GB-00013186.

XX (UYDU-) UNIV DUNDEE.

XX Alessi D, Biondi R, Komander D, Van AD;

XX WPI; 2004-062373/06.

XX Selecting/designing compound for modulating activity of phosphoinositide

PT dependent protein kinase 1 by using molecular modelling to select/design

PT compound predicted to interact with protein kinase catalytic domain.

XX Disclosure; Fig 7; 383pp; English.

XX The present invention describes a method (M1) for selecting or designing

CC a compound for modulating the activity of phosphoinositide dependent

CC protein kinase 1 (PDK1) comprising using molecular modelling means to

CC select or design a compound that is predicted to interact with the

CC protein kinase catalytic domain of PDK1, and selecting a compound that is

CC predicted to interact with the protein kinase catalytic domain. Also

CC described: (1) selecting or designing (M2) a compound for modulating the

CC activity of a hydrophobic pocket (PIF binding pocket)-containing protein

CC kinase having a hydrophobic pocket in the position equivalent to the

CC hydrophobic pocket of human PDK1 that is defined by residues including

CC Lys115, Ile118, Ile119, Val124, Val127 and/or Leu155 of full-length human

CC PDK1 and further having a phosphate binding pocket in the position

CC equivalent to the phosphate binding pocket of human PDK1 that is defined

CC by residues including Lys76, Arg131, Thr148 and/or Gln150; (2) assessing

CC (M3) the activation state of a structure for a protein kinase; (3) a

CC mutated protein kinase (I); (4) a polynucleotide (II) encoding (I); (5) a

CC host cell (III) comprising (II); (6) identifying (M4) a compound that

CC modulates the protein kinase activity of a protein kinase (e.g., PDK1);

CC (7) an antibody (IV) reactive with the phosphate binding pocket of PDK1

CC or (I) or an antibody reactive with PDK1 or (I) but not with the protein

CC kinase mutated at the phosphate binding site, or vice versa; (8) a

CC compound (V) identified or identifiable by (M1) or (M3); (9) use of (V),

CC (I), (II) in medicine; (10) use of (V), (I), (II) for the manufacture of

CC a medicament for the treatment of a patient in need of modulation of

CC signalling by a protein kinase as defined, for example PDK1, SGK, PKB, or

CC p70 S6 kinase, for example insulin signalling pathway and/or

CC PDK1/PDK2/SGK/PKB/p70 S6 kinase/PKB2/PKC signalling; and (11) a

CC crystalline form (VI) of polypeptide as defined in (M1). (I) has

CC antifungal, antidiabetic, cardiant, cytostatic, cerebroprotective,

CC vasotropic and anorectic activities, and can be used as a modulator of

CC protein kinase. (V) is useful for modulating the ability of protein

CC kinase to phosphorylate different substrates, e.g., different naturally

CC occurring polypeptides, to different extents. (V) inhibits or increases

CC the activity of protein kinase. The protein structures e.g., the co-

CC ordinates as provided in the specification are useful for designing

CC reagent useful in drug designing assays or characterisation of protein

CC kinase activity or regulation. (V) capable of producing the activity of

CC PKC, e.g., PKC beta, PKR1 or PKR2, PDK1, PKB, SGK or p70 S6 kinase, is

CC useful in treating cancer. (V) capable of increasing the activity of

CC PDK1, PKB, SGK or p70 S6 kinase is useful in treating diabetes or obesity

CC or may be useful in inhibiting apoptosis, thus useful in treating

CC diseases in which apoptosis is involved e.g., mechanical (including heat)

CC tissue injury or ischaemia disease such as stroke, myocardial infarction

CC and neural injury. (V) is useful as an antifungal agent. The present

CC sequence is used in the exemplification of the present invention.

XX Sequence 318 AA;

SQ

Query Match 94.4%; Score 51; DB 8; Length 318;

Best Local Similarity 75.0%; Pred. NO. 0.49;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXADE 13

Db 149 TFCGTIEYMAPE 160

RESULT 33

ABRS7464

ID ABR57464 standard; protein; 333 AA.

XX AC ABR57464;

XX DT 15-SEP-2003 (first entry)

XX DE AGC family protein kinase protein p70-S6K.

XX Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;

KW protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;

KW neotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;

KW structural analysis; cancer; diabetes; erectile dysfunction;

KW neurodegeneration.

XX Unidentified.

XX WO2003016516-A2.

XX PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-GB003735.

XX 14-AUG-2001; 2001GB-00019860.

PR 01-MAY-2002; 2002GB-00009985.

XX (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.

PA (CANC-) CANCER RES INST.

XX Barford D, Yang J, Hemmings BA, Cron PD;

XX WPI; 2003-268328/26.

XX New crystal of protein kinase B beta, useful for activating protein

PT kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates

PT or a tetragonal space group.

XX Disclosure; Fig 4; 284pp; English.

XX The present invention describes a crystal of protein kinase B beta

CC (PKBbeta) comprising (I), where (I) comprises: (a) a tetragonal space

CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus

CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or

CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40

CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =

CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom,

CC c = 39.19 plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5

CC Angstrom, b = 149.52 plus or minus 0.5 Angstrom, c = 39.06 plus or minus

CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in

CC the specification. (I) has cytostatic, antidiabetic, vasotropic,

CC neotropic and neuroprotective activities, and can be used in gene

CC therapy. The crystal of PKBbeta, and methods from the present invention,

CC are useful in activating protein kinases, particularly AGC kinases, for

CC identifying modulators of protein kinase activity, and for structural

CC analysis of other protein kinases. The crystal may also be used in

CC manufacturing a medicament for treating cancers, diabetes, erectile  
 CC dysfunction or neurodegeneration. The present sequence represents an AGC  
 CC family protein kinase which is given in the exemplification of the  
 CC present invention  
 XX  
 XX  
 SQ Sequence 333 AA;

Query Match 94.4%; Score 51; DB 6; Length 333;

Best Local Similarity 75.0%; Pred. No. 0.51;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 |||||  
 Db 168 TFCGTIEYMAPE 179

RESULT 34

AAV77845  
 ID AAY77845 standard; protein; 338 AA.

AC AAY77845;  
 XX  
 XX 19-JUN-2000 (first entry)  
 DT  
 XX Human serine/threonine protein kinase (HSTK)-3.  
 DE  
 XX Serine/threonine protein kinase; HSTK; cancer; leukemia; testicular;  
 KW melanoma; inflammatory disease; asthma; atherosclerosis; aniridia;  
 KW diabetes mellitus; growth disorder; anemia; achondroplastic dwarfism;  
 KW human; HSTK-3.  
 XX  
 XX Homo sapiens.

OS

XX WO200015770-A2.

XX 23-MAR-2000.

XX 16-SEP-1999; 99WO-US021595.

XX 16-SEP-1998; 98US-00153939.

XX (INCY-) INCYTE PHARM INC.

XX Bandnan O, Tang YT, Goli SK, Corley NC, Guegler KJ, Gorgone GA;  
 PI Hillman JL;

XX WPI; 2000-271413/23.

XX N-PSDB; AAZ87838.

XX Human serine/threonine protein kinases useful in the prevention,  
 PT diagnosis and treatment of cancers, inflammatory diseases and disorders  
 PT that affect growth and development.

XX Claim 1; Fig 2A-E; 73pp; English.

XX The invention relates to human serine/threonine protein kinase (HSTK)-3  
 CC polypeptides and the nucleic acids that encode them. The HSTK-3 protein  
 CC can be expressed by standard recombinant methodology. The HSTK-3  
 CC polypeptides may be used as antigens in the production of antibodies  
 CC against HSTK-3 and in assays to identify modulators (agonists and  
 CC antagonists) of HSTK-3 expression and activity. The HSTK-3 specific  
 CC antibodies and modulators can be used to treat disorders such as cancers  
 CC (e.g. leukemia, testicular cancer and melanomas), inflammatory diseases  
 CC (e.g. asthma, atherosclerosis and diabetes mellitus) and disorders that  
 CC affect growth and development (e.g. anemia, achondroplastic dwarfism and  
 CC aniridia). The anti-HSTK-3 antibodies may also be used as diagnostic  
 CC agents for detecting the presence of HSTK-3 polypeptides in samples (e.g.  
 CC by enzyme linked immunosorbant assay (ELISA)). The present sequence  
 CC represents the HSTK-3 polypeptide

XX Sequence 338 AA;

Query Match

94.4%; Score 51; DB 3; Length 338;

Best Local Similarity 75.0%; Pred. No. 0.51;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 |||||  
 Db 84 TFCGTIEYMAPE 95

RESULT 35

ADX91853  
 ID ADX91853 standard; protein; 342 AA.

XX  
 AC ADX91853;

XX 21-APR-2005 (first entry)

XX Plant full length insert polypeptide seqid 54517.

XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.

XX Unidentified.

XX US2004034888-A1.

XX 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

XX 05-NOV-2001; 2001US-00985678.

XX (LIU/) LIU J.

XX (ZHOU/) ZHOU Y.

XX (KOVA/) KOVALIC D K.

XX (SCRE/) SCREEN S E.

XX (TAB/) TABASKA J E.

XX (CAO/) CAO Y.

XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 PI WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.

XX Claim 1; SEQ ID NO 54517; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the

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CC invention.
XX
SQ Sequence 342 AA;

Query Match          94.4%; Score 51; DB 8; Length 342;
Best Local Similarity 75.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
   |||||
Db 69 TFCGTIEYNAPE 80

RESULT 36
ADP29809
ID ADP29809 standard; protein; 372 AA.
XX
AC ADP29809;
DT 12-AUG-2004 (first entry)
XX
DE Human secreted protein SEQ ID #576.
XX
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
PN WO2004035732-A2.
XX
PD 29-APR-2004.
XX
PF 28-AUG-2003; 2003WO-US026780.
XX
PR 29-AUG-2002; 2002US-0406576P.
PR 29-AUG-2002; 2002US-0406579P.
PR 29-AUG-2002; 2002US-0406585P.
PR 29-AUG-2002; 2002US-0406588P.
PR 29-AUG-2002; 2002US-0406608P.
PR 29-AUG-2002; 2002US-0406611P.
PR 29-AUG-2002; 2002US-0406612P.
PR 29-AUG-2002; 2002US-0406616P.
PR 29-AUG-2002; 2002US-0406640P.
PR 29-AUG-2002; 2002US-0406642P.
PR 29-AUG-2002; 2002US-0406646P.
PR 29-AUG-2002; 2002US-0406653P.
PR 29-AUG-2002; 2002US-0406655P.
PR 29-AUG-2002; 2002US-0406666P.
PR 17-SEP-2002; 2002US-0410946P.
PR 17-SEP-2002; 2002US-0410947P.
PR 17-SEP-2002; 2002US-0410948P.
PR 17-SEP-2002; 2002US-0410949P.
PR 17-SEP-2002; 2002US-0410953P.
PR 17-SEP-2002; 2002US-0410957P.
PR 17-SEP-2002; 2002US-0410958P.
PR 17-SEP-2002; 2002US-0410959P.
PR 17-SEP-2002; 2002US-0410960P.
PR 17-SEP-2002; 2002US-0410961P.
PR 17-SEP-2002; 2002US-0410962P.
PR 17-SEP-2002; 2002US-0411019P.
PR 17-SEP-2002; 2002US-0411022P.
PR 17-SEP-2002; 2002US-0411023P.
PR 17-SEP-2002; 2002US-0411024P.
PR 17-SEP-2002; 2002US-0411032P.
PR 17-SEP-2002; 2002US-0411035P.
PR 17-SEP-2002; 2002US-0411037P.
PR 17-SEP-2002; 2002US-0411041P.
PR 17-SEP-2002; 2002US-0411045P.
PR 17-SEP-2002; 2002US-0411046P.
PR 17-SEP-2002; 2002US-0411048P.
PR 17-SEP-2002; 2002US-0411052P.
PR 17-SEP-2002; 2002US-0411055P.
PR 17-SEP-2002; 2002US-0411073P.

PR 17-SEP-2002; 2002US-0411082P.
PR 17-SEP-2002; 2002US-0411010P.
PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.
PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX
PI Williams LT, Chu K, Lee E, Hestir K, Beurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
PT New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 1807; 428pp; English.
XX
CC The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
SQ Sequence 372 AA;

Query Match          94.4%; Score 51; DB 8; Length 372;
Best Local Similarity 75.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
   |||||
Db 100 TFCGTIEYNAPE 111

RESULT 37
ADP74016
ID ADP74016 standard; protein; 403 AA.
XX
AC ADP74016;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 43382.
```

XX KW plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.  
 XX Unidentified.  
 XX US2004034888-A1.  
 XX 19-FEB-2004.  
 XX 28-APR-2003; 2003US-00425114.  
 XX 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.  
 XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX Claim 1; SEQ ID NO 43382; 15pp; English.  
 PS The invention describes a recombinant DNA construct comprising a  
 XX polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX Sequence 403 AA;  
 SQ Query Match 94.4%; Score 51; DB 8; Length 403;  
 Best Local Similarity 75.0%; Pred. No. 0.6;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXYXAPE 13  
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 88 TFCGTPAYVAPE 99  
 Db ADX73686 standard; protein; 427 AA.  
 RESULT 38  
 ADX73686  
 ID ADX73686 standard; protein; 427 AA.  
 XX

AC ADX73686;  
 XX 21-APR-2005 (first entry)  
 XX Plant full length insert polypeptide seqid 43052.  
 XX plant protectant; plant growth regulant; gene therapy; plant;  
 KW recombinant DNA construct; physical array; plant breeding marker;  
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KW growth rate; cell cycle pathway; disease resistance;  
 KW galactomannan production; lignin production; plant growth regulator;  
 KW yield; plant growth; plant development; seed oil; protein yield;  
 KW protein content.  
 XX Unidentified.  
 XX US2004034888-A1.  
 XX 19-FEB-2004.  
 XX 28-APR-2003; 2003US-00425114.  
 XX 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX WPI; 2004-180133/17.  
 XX New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 XX Claim 1; SEQ ID NO 43052; 15pp; English.  
 PS The invention describes a recombinant DNA construct comprising a  
 XX polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX Sequence 427 AA;  
 SQ Query Match 94.4%; Score 51; DB 8; Length 427;  
 Best Local Similarity 75.0%; Pred. No. 0.64;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 TFCGTXXYXAPE 13  
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 76 TFCGTPAYVAPE 87  
 Db

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RESULT 39
AD71518
ID ADX71518 standard; protein; 439 AA.
XX
AC ADX71518;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polypeptide seqid 40884.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TAB/) TABASKA J E.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
WPI; 2004-180133/17.
XX
DR
XX
PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 40884; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 439 AA;
Query Match 94.4%; Score 51; DB 8; Length 439;
Best Local Similarity 75.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2 TFCGTXYYAPE 13
DB 199 TFCGTPAYVAPE 210
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RESULT 40
ADU66586
ID ADU66586 standard; protein; 445 AA.
XX
AC ADU66586;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human kinase and phosphatase (KPP), Incyte polypeptide ID: 7516533CD1.
XX
KW developmental disorder; proliferative disorders; growth disorder;
KW neurological disease; immune disorder; cardiovascular disease;
KW immunosuppressive; neuroprotective; antilipemic; cardiovascular-gen.;
KW cancer; cytostatic; gene therapy; kinase and phosphatase; KPP;
KW 7516533CD1.
XX
OS Homo sapiens.
XX
PN WO2004098539-A2.
XX
PD 18-NOV-2004.
XX
PF 24-MAR-2004; 2004WO-US009215.
XX
PR 30-APR-2003; 2003US-0467491P.
XX
PR 09-MAY-2003; 2003US-0469441P.
XX
PR 05-JUN-2003; 2003US-0476408P.
XX
PR 12-AUG-2003; 2003US-0494565P.
XX
PR 20-NOV-2003; 2003US-0524415P.
XX
PR 10-DEC-2003; 2003US-0528750P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Elliott VS, Khare R, Richardson TW, Marquis JP, Swarnakar A;
PI Hafalia AJA, Becha SD, Chawla NK, Baughn MR, Lee SY, Tran UK;
PI Yue H, Nguyen DB, Thornton MB, Gururajan R, Gandhi AR, Lu Y;
PI Yao MG, Li JX, Luo W, Lee EA, Forsythe LJ, Ison CH, Wilson AD;
PI Jin P;
XX
WPI; 2004-813977/80.
XX
DR N-PSDB; ADU66629.
XX
PT New kinases and phosphatases, useful for diagnosing, treating, or
PT preventing cardiovascular, immune system, neurological, lipid, cell
PT proliferative disorders, disorders affecting growth and development, or
PT cancers.
XX
PS Claim 1; SEQ ID NO 10; 299pp; English.
XX
CC The invention relates to novel isolated human kinase and phosphatase
CC (KPP) polypeptides and their encoding polynucleotides. The KPP
CC polypeptide comprises any of the 43 sequences of 80-1355 amino acids (SEQ
CC ID NOS: 1-43) encoded by a polynucleotide comprising any of the 43
CC nucleotide sequences of 669-8015 bp (SEQ ID NOS: 44-86). The invention
CC further comprises: a transgenic organism comprising a recombinant KPP
CC polynucleotide; antibodies which specifically binds to the KPP
CC polypeptide; a method of detecting KPP target polynucleotides; method of
CC screening a compound as an agonist or as an antagonist of the KPP
CC polypeptide; a composition comprising the KPP polypeptide, an agonist or
CC an antagonist compound, an antibody and a pharmaceutical excipient; and a
CC method for treating a disease or condition associated with decreased
CC expression of functional kinases and phosphatases. The KPP polypeptides,
CC polynucleotides, compositions, and methods have the following activities:
CC cardiovascular-Gen, immunosuppressive, neuroprotective, antilipemic, and
CC cytostatic. The KPP polynucleotides may be used in gene therapy. The KPP
CC polypeptides, polynucleotides, compositions, and methods are useful for
CC diagnosing, treating, or preventing disorders with aberrant expression of

```

CC KPP, such as cardiovascular disease, immune system disorders,  
CC neurological disorders, disorders affecting growth and development, lipid  
CC disorders, cell proliferative disorders, or cancers. This sequence  
CC represents a human kinase and phosphatase (KPP) polypeptide of the  
CC invention.  
XX

SQ Sequence 445 AA;

Query Match 94.4%; Score 51; DB 8; Length 445;  
Best Local Similarity 75.0%; Pred. No. 0.86;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13

|||||

Db 172 TFCGTIEYMAPE 183

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Job time : 209.211 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)  
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Title: US-09-868-131C-48

Perfect score: 54

Sequence: 1 XTFCGTXXYXPE 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	96.3	376	2	US-09-248-796A-20505
2	52	96.3	513	2	US-09-248-796A-18515
3	52	96.3	776	1	US-08-198-446B-17
4	52	96.3	776	1	US-08-870-693-17
5	52	96.3	821	1	US-08-198-446B-6
6	52	96.3	821	1	US-08-870-693-6
7	52	96.3	824	2	US-09-487-558B-312
8	51	94.4	258	2	US-09-430-564-6
9	51	94.4	268	2	US-09-430-564-12
10	51	94.4	482	2	US-09-430-564-2
11	51	94.4	495	2	US-09-430-564-3
12	51	94.4	495	2	US-09-762-258-2
13	51	94.4	502	2	US-09-538-092-996
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15	51	94.4	525	1	US-08-749-902-8
16	51	94.4	525	2	US-09-430-564-16
17	51	94.4	525	2	US-09-762-258-4
18	51	94.4	637	2	US-09-817-310-2
19	51	94.4	637	2	US-10-355-724A-2
20	50	92.6	36	2	US-09-205-658-99
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22	50	92.6	43	2	US-09-205-658-207
23	50	92.6	45	2	US-08-857-076-62
24	50	92.6	45	2	US-08-857-076-91
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29	50	92.6	45	2	US-09-205-658-203
30	50	92.6	45	2	US-09-205-658-205
31	50	92.6	62	2	US-09-205-658-206
32	50	92.6	177	2	US-09-205-658-305
33	50	92.6	177	2	US-09-270-767-45660
34	50	92.6	263	1	US-07-857-224B-13
35	50	92.6	264	1	US-07-857-224B-9
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47	50	92.6	330	2	US-09-949-016-9369
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49	50	92.6	358	2	US-10-438-339-5
50	50	92.6	362	2	US-09-691-861A-4
51	50	92.6	407	2	US-10-067-977-4
52	50	92.6	417	2	US-09-590-740-4
53	50	92.6	430	1	US-08-712-709-9
54	50	92.6	430	2	US-09-111-444-9
55	50	92.6	430	2	US-09-541-228-9
56	50	92.6	431	1	US-08-712-709-5
57	50	92.6	431	2	US-09-111-444-5
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63	50	92.6	465	2	US-09-526-043-2
64	50	92.6	470	2	US-09-248-796A-18482
65	50	92.6	479	2	US-09-771-161A-246
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70	50	92.6	480	2	US-09-590-740-6
71	50	92.6	480	2	US-09-538-092-1053
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77	50	92.6	483	2	US-09-205-658-156
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79	50	92.6	546	2	US-09-205-658-155
80	50	92.6	568	2	US-09-949-016-7970
81	50	92.6	582	2	US-09-949-016-7830
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88	50	92.6	672	2	US-10-092-138A-27
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93	50	92.6	676	2	US-09-771-161A-209
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96	50	92.6	686	2	US-09-538-092-927
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Sequence 92, Appl  
Sequence 203, App  
Sequence 205, App  
Sequence 206, App  
Sequence 305, App  
Sequence 45660, A  
Sequence 13, Appl  
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Sequence 10, Appl  
Sequence 12, Appl  
Sequence 15, Appl  
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Sequence 7, Appl  
Sequence 6, Appl  
Sequence 9, Appl  
Sequence 14, Appl  
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Sequence 31, Appl  
Sequence 30, Appl  
Sequence 9369, Ap  
Sequence 157, App  
Sequence 5, Appl  
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Sequence 6, Appl  
Sequence 1053, Ap  
Sequence 157, App  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 223, App  
Sequence 1054, Ap  
Sequence 156, App  
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Sequence 7830, Ap  
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Sequence 7547, Ap  
Sequence 11676, A  
Sequence 5, Appl  
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Sequence 27, Appl  
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Sequence 2, Appl  
Sequence 209, App  
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Sequence 11575, A  
Sequence 927, App  
Sequence 1266, Ap  
Sequence 6710, Ap  
Sequence 7346, Ap  
Sequence 71, Appl

## ALIGNMENTS

## RESULT 1

US-09-248-796A-20505  
; Sequence 20505, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 20505  
; LENGTH: 376  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-20505

Query Match 96.3%; Score 52; DB 2; Length 376;  
Best Local Similarity 75.0%; Pred. No. 0.059;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
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Db 141 TFCGTTEYLAPE 152

## RESULT 2

US-09-248-796A-18515  
; Sequence 18515, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; PRIOR FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 18515  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-18515

Query Match 96.3%; Score 52; DB 2; Length 513;  
Best Local Similarity 75.0%; Pred. No. 0.08;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
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Db 360 TFCGTLAYVAPE 371

## RESULT 3

US-08-198-446B-17  
; Sequence 17, Application US/08198446B  
; Patent No. 5674996  
; GENERAL INFORMATION:  
; APPLICANT: Hartwell, Leland H.

; APPLICANT: Weinert, Ted A.  
; APPLICANT: Plon, Sharon E.  
; APPLICANT: Groudine, Mark T.  
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/198,446B  
; FILING DATE: 18-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sheiness, Diana K.  
; REGISTRATION NUMBER: 35,356  
; REFERENCE/DOCKET NUMBER: FHCRI7537  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-682-8100  
; TELEFAX: 206-224-0779  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 776 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; DESCRIPTION: Yeast MEC2 protein  
US-08-198-446B-17

Query Match 96.3%; Score 52; DB 1; Length 776;  
Best Local Similarity 75.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
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Db 354 TFCGTLAYVAPE 365

## RESULT 4

US-08-870-693-17  
; Sequence 17, Application US/08870693  
; Patent No. 5866338  
; GENERAL INFORMATION:  
; APPLICANT: Hartwell, Leland H.  
; APPLICANT: Weinert, Ted A.  
; APPLICANT: Plon, Sharon E.  
; APPLICANT: Groudine, Mark T.  
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC  
; STREET: 1420 Fifth Ave., Suite 2800  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101-2347  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/870,693  
; FILING DATE:  
; CLASSIFICATION: 536

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,446
; FILING DATE: February 18, 1994
; APPLICATION NUMBER: PCT/US93/04458
; FILING DATE: May 12, 1993
; APPLICATION NUMBER: US 07/884,426
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: US 07/882,051
; FILING DATE: May 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCR110798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: yeast MEC2 protein
;
US-08-870-693-17

Query Match          96.3%; Score 52; DB 1; Length 776;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
        |||||
Db      354 TFCGTLAYVAPE 365

RESULT 5
US-08-198-446B-6
; Sequence 6, Application US/08198446B
; Patent No. 5674996
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Plon, Sharon E.
; APPLICANT: Groudine, Mark T.
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/198,446
; FILING DATE: February 18, 1994
; APPLICATION NUMBER: PCT/US93/04458
; FILING DATE: May 12, 1993
; APPLICATION NUMBER: US 07/884,426
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: US 07/882,051
; FILING DATE: May 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCR110798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 821 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: yeast MEC2 protein
;
US-08-870-693-17

Query Match          96.3%; Score 52; DB 1; Length 821;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
        |||||
Db      354 TFCGTLAYVAPE 365

RESULT 6
US-08-870-693-6
; Sequence 6, Application US/08870693
; Patent No. 5866338
; GENERAL INFORMATION:
; APPLICANT: Hartwell, Leland H.
; APPLICANT: Weinert, Ted A.
; APPLICANT: Plon, Sharon E.
; APPLICANT: Groudine, Mark T.
; TITLE OF INVENTION: Cell Cycle Checkpoint Genes
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/870,693
; FILING DATE: May 12, 1992
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,446
; FILING DATE: February 18, 1994
; APPLICATION NUMBER: PCT/US93/04458
; FILING DATE: May 12, 1993
; APPLICATION NUMBER: US 07/884,426
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: US 07/882,051
; FILING DATE: May 12, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheiness, Diana K.
; REGISTRATION NUMBER: 35,356
; REFERENCE/DOCKET NUMBER: FHCR110798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-682-8100
; TELEFAX: 206-224-0779
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 821 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: yeast MEC2 protein
;
US-08-870-693-6

Query Match          96.3%; Score 52; DB 1; Length 821;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
        |||||
Db      354 TFCGTLAYVAPE 365
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Db 354 TFCGTLAYVAPE 365

```
RESULT 7
US-09-487-558B-312
; Sequence 312, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 312
; LENGTH: 824
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-312
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Query Match 96.3%; Score 52; DB 2; Length 824;
Best Local Similarity 75.0%; Pred. No. 0.13; 3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
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QY 2 TFCGTXXYXAPE 13  
|||||

Db 570 TFCGTTEYLAPE 581

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RESULT 8
US-09-430-564-6
; Sequence 6, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-6
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Query Match 94.4%; Score 51; DB 2; Length 258;
Best Local Similarity 75.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 TFCGTXXYXAPE 13  
|||||

Db 164 TFCGTIEYMAPE 175

```
RESULT 9
US-09-430-564-12
; Sequence 12, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-12
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```
Query Match 94.4%; Score 51; DB 2; Length 268;
Best Local Similarity 75.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 2 TFCGTXXYXAPE 13  
|||||

Db 164 TFCGTIEYMAPE 175

```
RESULT 10
US-09-430-564-2
; Sequence 2, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-2
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Query Match 94.4%; Score 51; DB 2; Length 482;
Best Local Similarity 75.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 2 TFCGTXXYXAPE 13  
|||||

Db 228 TFCGTIEYMAPE 239

```
RESULT 11
US-09-430-564-3
; Sequence 3, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
```

; APPLICANT: Kay K. Lee-Fruman  
; APPLICANT: Calvin J. Kuo  
; TITLE OF INVENTION: P54S6K AND P55S6K GENES, PROTEINS,  
; FILE REFERENCE: 00246/506002  
; CURRENT APPLICATION NUMBER: US/09/430,564  
; CURRENT FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: 60/106,141  
; PRIOR FILING DATE: 1998-10-29  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-430-564-3

Query Match 94.4%; Score 51; DB 2; Length 495;  
Best Local Similarity 75.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 241 TFCGTIEYMAPE 252

RESULT 12  
US-09-762-258-2  
; Sequence 2, Application US/09762258  
; Patent No. 6830909  
; GENERAL INFORMATION:  
; APPLICANT: Gout, Ivan  
; APPLICANT: Hara, Kenta  
; APPLICANT: Waterfield, Michael  
; APPLICANT: Yonezawa, Kazu  
; TITLE OF INVENTION: Identification and Functional Characterization of a  
; TITLE OF INVENTION: No. 6830909el Ribosomal S6 Protein Kinase  
; FILE REFERENCE: 40750-5002-US  
; CURRENT APPLICATION NUMBER: US/09/762,258  
; CURRENT FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: PCT/US99/17595  
; PRIOR FILING DATE: 1999-08-04  
; PRIOR APPLICATION NUMBER: 60/095,268  
; PRIOR FILING DATE: 1998-08-04  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: p70 (beta) S6 Kinase protein  
US-09-762-258-2

Query Match 94.4%; Score 51; DB 2; Length 495;  
Best Local Similarity 75.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 241 TFCGTIEYMAPE 252

RESULT 13  
US-09-538-092-996  
; Sequence 996, Application US/09538092  
; Patent No. 6753314  
; GENERAL INFORMATION:  
; APPLICANT: Giot, Loic  
; APPLICANT: Mansfield, Traci A.  
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092  
; CURRENT FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 60/127,352  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: 60/178,965  
; PRIOR FILING DATE: 2000-02-01  
; NUMBER OF SEQ ID NOS: 1387  
; SOFTWARE: CuraPatSeqFormatter Version 0.9  
; SEQ ID NO 996  
; LENGTH: 502  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (0)\_(0)  
; OTHER INFORMATION: Polypeptide Accession Number P23443  
US-09-538-092-996

Query Match 94.4%; Score 51; DB 2; Length 502;  
Best Local Similarity 75.0%; Pred. No. 0.12;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 229 TFCGTIEYMAPE 240

RESULT 14  
US-08-749-902-7  
; Sequence 7, Application US/08749902  
; Patent No. 5985635  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Hillman, Jennifer L.  
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE  
; TITLE OF INVENTION: PROTEIN KINASES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/749,902  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0150 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 525 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 189508  
US-08-749-902-7

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Query Match          94.4%; Score 51; DB 1; Length 525;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
Db      252 TFCGTIEYMAPE 263

RESULT 15
US-08-749-902-8
; Sequence 8, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 525 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1562
US-08-749-902-8

Query Match          94.4%; Score 51; DB 1; Length 525;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
Db      252 TFCGTIEYMAPE 263

RESULT 16
US-09-430-564-16
; Sequence 16, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Pruman

; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
; TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
; FILE REFERENCE: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-564-16

Query Match          94.4%; Score 51; DB 2; Length 525;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
Db      252 TFCGTIEYMAPE 263

RESULT 17
US-09-762-258-4
; Sequence 4, Application US/09762258
; Patent No. 6830909
; GENERAL INFORMATION:
; APPLICANT: Gout, Ivan
; APPLICANT: Hara, Kenta
; APPLICANT: Waterfield, Michael
; APPLICANT: Yonezawa, Kazu
; APPLICANT: Ludwig Institute for Cancer Research
; TITLE OF INVENTION: Identification and Functional Characterization of a
; TITLE OF INVENTION: No. 6830909e1 Ribosomal S6 Protein Kinase
; FILE REFERENCE: 40750-5002-US
; CURRENT APPLICATION NUMBER: US/09/762,258
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: PCT/US99/17595
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/095,268
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: p70(alpha) S6 Kinase protein
US-09-762-258-4

Query Match          94.4%; Score 51; DB 2; Length 525;
Best Local Similarity 75.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
Db      252 TFCGTIEYMAPE 263

RESULT 18
US-09-817-310-2
; Sequence 2, Application US/09817310
; Patent No. 6534311
; GENERAL INFORMATION:
; APPLICANT: Stewart, Mary
; APPLICANT: Kozma, Sarah
; APPLICANT: Thomas, George
; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
; FILE REFERENCE: 4-20971/A
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; CURRENT APPLICATION NUMBER: US/09/817,310
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 09/230,247
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-817-310-2

Query Match          94.4%; Score 51; DB 2; Length 637;
Best Local Similarity 75.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
Db 238 TFCGTIEYMAPE 249

RESULT 19
US-10-355-724A-2
; Sequence 2, Application US/10355724A
; Patent No. 6833255
; GENERAL INFORMATION:
; APPLICANT: Stewart, Mary
; APPLICANT: Kozma, Sarah
; APPLICANT: Thomas, George
; TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
; FILE REFERENCE: 4-20971/A
; CURRENT APPLICATION NUMBER: US/10/355,724A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: GB 96/5498.4
; PRIOR FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-355-724A-2

Query Match          94.4%; Score 51; DB 2; Length 637;
Best Local Similarity 75.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
Db 238 TFCGTIEYMAPE 249

RESULT 20
US-09-205-658-99
; Sequence 99, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99

Query Match          92.6%; Score 50; DB 2; Length 36;
Best Local Similarity 75.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
Db 24 TFCGTPEYLAPE 35

RESULT 21
US-09-205-658-204
; Sequence 204, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens or Caenorhabditis elegans
US-09-205-658-204

Query Match          92.6%; Score 50; DB 2; Length 36;
Best Local Similarity 75.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
Db 24 TFCGTPEYLAPE 35

RESULT 22
US-09-205-658-207
; Sequence 207, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: 00786/351004
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans or Mus musculus
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US-09-205-658-207

Query Match 92.6%; Score 50; DB 2; Length 43;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||  
Db 7 TFCGTPEYLAPE 18

RESULT 23

US-08-857-076-62  
; Sequence 62, Application US/08857076C  
; Patent No. 6225120  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Kimura, Koutarou  
; APPLICANT: Patterson, Garth  
; APPLICANT: Ogg, Scott  
; APPLICANT: Paradis, Suzanne  
; APPLICANT: Tissenbaum, Heidi  
; APPLICANT: Morris, Jason  
; APPLICANT: Kweek, Allison  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351001  
; CURRENT APPLICATION NUMBER: US/08/857,076C  
; CURRENT FILING DATE: 1997-05-15  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-08-857-076-62

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 24

US-08-857-076-91  
; Sequence 91, Application US/08857076C  
; Patent No. 6225120  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Kimura, Koutarou  
; APPLICANT: Patterson, Garth  
; APPLICANT: Ogg, Scott  
; APPLICANT: Paradis, Suzanne  
; APPLICANT: Tissenbaum, Heidi  
; APPLICANT: Morris, Jason  
; APPLICANT: Kweek, Allison  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351001  
; CURRENT APPLICATION NUMBER: US/08/857,076C  
; CURRENT FILING DATE: 1997-05-15  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-857-076-91

Query Match 92.6%; Score 50; DB 2; Length 45;

Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 25

US-08-857-076-92  
; Sequence 92, Application US/08857076C  
; Patent No. 6225120  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Kimura, Koutarou  
; APPLICANT: Patterson, Garth  
; APPLICANT: Ogg, Scott  
; APPLICANT: Paradis, Suzanne  
; APPLICANT: Tissenbaum, Heidi  
; APPLICANT: Morris, Jason  
; APPLICANT: Kweek, Allison  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351001  
; CURRENT APPLICATION NUMBER: US/08/857,076C  
; CURRENT FILING DATE: 1997-05-15  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-08-857-076-92

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 26

US-09-205-658-62  
; Sequence 62, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; EARLIER FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 62  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-205-658-62

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;



QY 2 TFCGTXXYXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 27  
US-09-205-658-91  
; Sequence 91, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-205-658-91

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 28  
US-09-205-658-92  
; Sequence 92, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 92  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-205-658-92

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 29  
US-09-205-658-203  
; Sequence 203, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 203  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-205-658-203

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 30  
US-09-205-658-205  
; Sequence 205, Application US/09205658  
; Patent No. 6861256  
; GENERAL INFORMATION:  
; APPLICANT: Ruvkun, Gary  
; APPLICANT: Ogg, Scott  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
; FILE REFERENCE: 00786/351004  
; CURRENT APPLICATION NUMBER: US/09/205,658  
; CURRENT FILING DATE: 1998-12-03  
; EARLIER APPLICATION NUMBER: 08/857,076  
; EARLIER FILING DATE: 1997-05-15  
; EARLIER APPLICATION NUMBER: 08/888,534  
; EARLIER FILING DATE: 1997-07-07  
; EARLIER APPLICATION NUMBER: US98/10080  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 205  
; LENGTH: 45  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-205-658-205

Query Match 92.6%; Score 50; DB 2; Length 45;  
Best Local Similarity 75.0%; Pred. No. 0.017;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 33 TFCGTPEYLAPE 44

RESULT 31

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US-09-205-658-206
; Sequence 206, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-206

Query Match          92.6%; Score 50; DB 2; Length 62;
Best Local Similarity 75.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
DB      14 TFCGTPEYLAPE 25

RESULT 32
US-09-205-658-305
; Sequence 305, Application US/09205658
; Patent No. 6861256
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: US98/10080
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-205-658-305

Query Match          92.6%; Score 50; DB 2; Length 62;
Best Local Similarity 75.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
DB      14 TFCGTPEYLAPE 25

RESULT 33
US-09-270-767-45660
; Sequence 45660, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45660
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45660

Query Match          92.6%; Score 50; DB 2; Length 177;
Best Local Similarity 75.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      ||||| |||
DB      159 TFCGTPEYLAPE 170

RESULT 34
US-07-857-224B-13
; Sequence 13, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: rabbit
; FEATURE: Protein kinase: Table 8 Column 14
; PUBLICATION INFORMATION:
; AUTHORS:
; AUTHORS: Hanks, S. K.
; AUTHORS: Quinn, A. M.
; AUTHORS: Hunter, T.
; TITLES: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
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; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: bovine
; FEATURE: Protein kinase; Table 8 Column 13
; PUBLICATION INFORMATION:
; AUTHORS:
; HANKS, S. K.
; QUINN, A. M.
; HUNTER, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
;
; US-07-857-224B-12
;
; Query Match 92.6%; Score 50; DB 1; Length 264;
; Best Local Similarity 75.0%; Pred. No. 0.098;
; Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 TFCGTXXYXAPE 13
; ||||| |||
; Db 161 TFCGTPDYIAPE 172
;
; RESULT 38
; US-07-857-224B-15
; Sequence 15, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; FEATURE: Protein kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
```

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; TELEFAX: (International) 41 1 262 2437
; TELEX: none
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: bovine
; FEATURE: Protein kinase; Table 8 Column 16
; PUBLICATION INFORMATION:
; AUTHORS:
; HANKS, S. K.
; QUINN, A. M.
; HUNTER, T.
; TITLE: The protein kinase family
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
;
; US-07-857-224B-15
;
; Query Match 92.6%; Score 50; DB 1; Length 264;
; Best Local Similarity 75.0%; Pred. No. 0.098;
; Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 TFCGTXXYXAPE 13
; ||||| |||
; Db 161 TFCGTPDYIAPE 172
;
; RESULT 39
; US-07-857-224B-17
; Sequence 17, Application US/07857224B
; Patent No. 5958784
; GENERAL INFORMATION:
; APPLICANT: Benner, Steven A.
; TITLE OF INVENTION: Predicting Folded Structures of Proteins
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: Hadlaubstrasse 151
; CITY: Zurich
; STATE: none
; COUNTRY: Switzerland
; ZIP: (note: this is an international post code) CH-8092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/857,224B
; FILING DATE: 03/25/92
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA: none
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
; TELEFAX: (International) 41 1 262 2437
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; FEATURE: Protein kinase; Table 8 Column 18
; PUBLICATION INFORMATION:
; TELEPHONE: (International) 41 1 632 2830
```

; AUTHORS: Hanks, S. K.  
 ; AUTHORS: Quinn, A. M.  
 ; AUTHORS: Hunter, T.  
 ; TITLE: The protein kinase C  
 ; JOURNAL: Science  
 ; VOLUME: 241  
 ; PAGES: 42-52  
 ; DATE: 1988  
 ; US-07-857-224B-17

Query Match 92.6%; Score 50; DB 1; Length 264;  
Best Local Similarity 75.0%; Pred. No. 0.098;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TFCGTXXYXAPE 13  
| | | | |  
Db 161 TFCGTPDYIAPE 172

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RESULT 40
US-09-797-908-7
; Sequence 7, Application US/09797908
; Patent No. 6555352
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL00781
; CURRENT APPLICATION NUMBER: US/09/797,908
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-797-908-7

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Query Match      92.6%; Score 50; DB 2; Length.267;
Best Local Similarity 66.7%; Pred. No. 0.099;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Qy 2 TFCGTXXYXAPE 13  
|||: |||  
Db 170 TFCGSAAYAAPE 181

Search completed: February 18, 2006, 08:02:59  
Job time : 46.1579 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 08:16:49 ; Search time 159.421 Seconds  
(without alignments)  
34.072 Million cell updates/sec

Title: US-09-868-131C-48  
Perfect score: 54  
Sequence: 1 XTCGTXXXAPE 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	96.3	375	4	US-10-116-722A-1
2	52	96.3	428	5	US-10-732-923-10735
3	52	96.3	494	4	US-10-369-493-12679
4	52	96.3	523	3	US-09-740-627-11
5	52	96.3	527	6	US-11-007-819-27
6	52	96.3	534	4	US-10-369-493-3090
7	52	96.3	581	4	US-10-369-493-6075
8	52	96.3	646	4	US-10-369-493-2280
9	52	96.3	699	4	US-10-032-585-7635
10	52	96.3	728	4	US-10-369-493-2214
11	52	96.3	821	4	US-10-081-119-16
12	52	96.3	821	5	US-10-951-389-16
13	52	96.3	821	5	US-10-951-406-16
14	52	96.3	821	5	US-10-951-477-16
15	52	96.3	821	5	US-10-977-087-16
16	52	96.3	823	4	US-10-369-493-22067
17	52	96.3	824	3	US-09-801-368-312
18	52	96.3	917	5	US-10-732-923-10691
19	52	96.3	919	5	US-10-732-923-10655
20	51	94.4	12	4	US-10-148-786A-42
21	51	94.4	198	4	US-10-240-315-4
22	51	94.4	281	4	US-10-220-955-13
23	51	94.4	299	4	US-10-425-115-222617
24	51	94.4	310	6	US-11-007-819-39
25	51	94.4	311	4	US-10-369-493-3875
26	51	94.4	333	4	US-10-217-574-16
27	51	94.4	333	4	US-10-217-555-16
28	51	94.4	342	4	US-10-425-114-54517
29	51	94.4	368	6	US-11-007-819-33
30	51	94.4	392	6	US-11-007-819-35
31	51	94.4	403	4	US-10-425-114-43382
32	51	94.4	427	4	US-10-425-114-43052
33	51	94.4	439	4	US-10-425-114-40884
34	51	94.4	460	3	US-09-740-627-10
35	51	94.4	464	4	US-10-369-493-12994
36	51	94.4	469	4	US-10-425-114-57769
37	51	94.4	475	6	US-10-424-599-269103
38	51	94.4	475	6	US-11-007-819-20
39	51	94.4	483	6	US-11-007-819-43
40	51	94.4	489	6	US-11-007-819-8
41	51	94.4	490	6	US-11-007-819-41
42	51	94.4	490	6	US-11-097-143-22083
43	51	94.4	495	6	US-11-004-840-2
44	51	94.4	502	4	US-10-316-253-32
45	51	94.4	502	4	US-10-425-114-54060
46	51	94.4	502	6	US-11-007-819-47
47	51	94.4	508	4	US-10-437-963-129122
48	51	94.4	508	6	US-11-007-819-4
49	51	94.4	510	6	US-11-007-819-6
50	51	94.4	511	4	US-10-437-963-125840
51	51	94.4	516	6	US-11-007-819-37
52	51	94.4	517	6	US-11-007-819-16
53	51	94.4	518	4	US-10-425-115-338791
54	51	94.4	518	6	US-11-007-819-10
55	51	94.4	518	6	US-11-007-819-14
56	51	94.4	518	6	US-11-007-819-26
57	51	94.4	519	6	US-11-007-819-24
58	51	94.4	520	6	US-11-007-819-45
59	51	94.4	520	6	US-11-007-819-51
60	51	94.4	521	6	US-11-007-819-2
61	51	94.4	522	5	US-10-732-923-10757
62	51	94.4	525	4	US-10-316-253-34
63	51	94.4	525	5	US-10-739-930-10572
64	51	94.4	525	5	US-11-004-840-4
65	51	94.4	528	4	US-10-424-599-146411
66	51	94.4	528	6	US-11-007-819-18
67	51	94.4	538	4	US-10-437-963-130054
68	51	94.4	541	4	US-10-424-599-146409
69	51	94.4	541	4	US-10-425-114-43778
70	51	94.4	554	4	US-10-425-114-52763
71	51	94.4	609	4	US-10-369-493-22674
72	51	94.4	637	3	US-09-817-310-2
73	50	92.6	12	4	US-10-148-786A-38
74	50	92.6	12	4	US-10-148-786A-39
75	50	92.6	12	4	US-10-148-786A-40
76	50	92.6	14	4	US-10-148-786A-4
77	50	92.6	16	4	US-10-148-786A-6
78	50	92.6	16	4	US-10-148-786A-27
79	50	92.6	20	6	US-11-022-327-66
80	50	92.6	35	4	US-10-380-235-33
81	50	92.6	35	4	US-10-380-235-35
82	50	92.6	36	3	US-09-205-658-99
83	50	92.6	36	3	US-09-205-658-204
84	50	92.6	36	3	US-09-963-693-99
85	50	92.6	36	3	US-09-963-693-204
86	50	92.6	39	4	US-10-148-786A-3
87	50	92.6	39	4	US-10-148-786A-34
88	50	92.6	39	5	US-10-994-093-13
89	50	92.6	39	5	US-10-922-337-9
90	50	92.6	42	3	US-09-864-761-43465
91	50	92.6	43	3	US-09-205-658-207
92	50	92.6	43	3	US-09-963-693-202
93	50	92.6	45	3	US-09-205-658-62
94	50	92.6	45	3	US-09-205-658-91
95	50	92.6	45	3	US-09-205-658-92
96	50	92.6	45	3	US-09-205-658-203
97	50	92.6	45	3	US-09-205-658-205
98	50	92.6	45	3	US-09-844-353A-62
99	50	92.6	45	3	US-09-844-353A-91
100	50	92.6	45	3	US-09-844-353A-92

## ALIGNMENTS

RESULT 1  
US-10-116-722A-1  
; Sequence 1, Application US/10116722A  
; Publication No. US20030044946A1  
; GENERAL INFORMATION:  
; APPLICANT: LONGO, VALTER D.  
; TITLE OF INVENTION: GENES, MUTATIONS, AND DRUGS THAT INCREASE CELLULAR  
; TITLE OF INVENTION: RESISTANCE TO DAMAGE AND EXTEND LONGEVITY IN ORGANISMS  
; TITLE OF INVENTION: FROM YEAST TO HUMANS  
; FILE REFERENCE: 13761-7068  
; CURRENT APPLICATION NUMBER: US/10/116,722A  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: 60/281,213  
; PRIOR FILING DATE: 2001-04-03  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Saccharomyces sp.  
US-10-116-722A-1

Query Match 96.3%; Score 52; DB 4; Length 375;  
Best Local Similarity 75.0%; Pred. No. 0.18;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 208 TFCGTTTSLAPE 219

RESULT 2  
US-10-732-923-10735  
; Sequence 10735, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 10735  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Trypanosoma cruzi  
US-10-732-923-10735

Query Match 96.3%; Score 52; DB 5; Length 428;  
Best Local Similarity 75.0%; Pred. No. 0.21;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 260 TFCGTTTSLAPE 271

RESULT 3  
US-10-369-493-12679  
; Sequence 12679, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 12679  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Aspergillus nidulans  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(494)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-12679

Query Match 96.3%; Score 52; DB 4; Length 494;  
Best Local Similarity 75.0%; Pred. No. 0.24;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 318 TFCGTTTSLAPE 329

RESULT 4  
US-09-740-627-11  
; Sequence 11, Application US/09740627  
; Patent No. US20020012964A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakanishi, Makoto  
; TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR  
; FILE REFERENCE: 06501-071001  
; CURRENT APPLICATION NUMBER: US/09/740,627  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: PCT/JP99/03350  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: JP 10/192467  
; PRIOR FILING DATE: 1998-06-23  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-740-627-11

Query Match 96.3%; Score 52; DB 3; Length 522;  
Best Local Similarity 75.0%; Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 354 TFCGTTTSLAPE 365

RESULT 5  
US-11-007-819-27  
; Sequence 27, Application US/11007819  
; Publication No. US20050235377A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; APPLICANT: Dasgupta, Santanu  
; APPLICANT: Jayaprakash, T.L.  
; APPLICANT: Thal, Carolyn J.  
; APPLICANT: Narayanan, K.K.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Dotson, Stanton B.  
; TITLE OF INVENTION: OapK7  
; FILE REFERENCE: 38-21(53203)B



; CURRENT APPLICATION NUMBER: US/11/007,819  
; CURRENT FILING DATE: 2004-12-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 27  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-11-007-819-27

Query Match 96.3%; Score 52; DB 6; Length 527;  
Best Local Similarity 75.0%; Pred. No. 0.25;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
|||||  
Db 202 TFCGTRAYVAPE 213

## RESULT 6

US-10-369-493-3090  
; Sequence 3090, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 3090  
; LENGTH: 554  
; TYPE: PRT  
; ORGANISM: Neurospora crassa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(554)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-3090

Query Match 96.3%; Score 52; DB 4; Length 554;  
Best Local Similarity 75.0%; Pred. No. 0.26;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
|||||  
Db 367 TFCGTTEYLAPE 378

## RESULT 7

US-10-369-493-6075  
; Sequence 6075, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 6075  
; LENGTH: 581  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-10-369-493-6075

Query Match 96.3%; Score 52; DB 4; Length 581;  
Best Local Similarity 75.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
|||||  
Db 429 TFCGTAEVVAPE 440

## RESULT 8

US-10-369-493-2280  
; Sequence 2280, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2280  
; LENGTH: 646  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
US-10-369-493-2280

Query Match 96.3%; Score 52; DB 4; Length 646;  
Best Local Similarity 75.0%; Pred. No. 0.3;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13  
|||||  
Db 426 TFCGTTDYLAPE 437

## RESULT 9

US-10-032-585-7635  
; Sequence 7635, Application US/10032585  
; Publication No. US20030180953A1  
; GENERAL INFORMATION:  
; APPLICANT: Terry, Roemer D.  
; APPLICANT: Bo, Jiang  
; APPLICANT: Charles, Boone  
; APPLICANT: Howard, Bussey  
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery  
; FILE REFERENCE: 10182-005-999  
; CURRENT APPLICATION NUMBER: US/10/032,585  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 8000  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 7635  
; LENGTH: 699  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-10-032-585-7635

Query Match 96.3%; Score 52; DB 4; Length 699;  
Best Local Similarity 75.0%; Pred. No. 0.33;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||.|||||  
Db 331 TFCGTLAYVAPE 342

RESULT 10  
US-10-369-493-2214  
; Sequence 2214, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 2214  
; LENGTH: 768  
; TYPE: PRT  
; ORGANISM: Schizosaccharomyces pombe  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(768)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-2214

Query Match 96.3%; Score 52; DB 4; Length 768;  
Best Local Similarity 75.0%; Pred. No. 0.36;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||.|||||  
Db 517 TFCGTTEYLAPE 528

RESULT 11  
US-10-081-119-16  
; Sequence 16, Application US/10081119  
; Publication No. US20030045491A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
; TITLE OF INVENTION: Target in Cancer  
; FILE REFERENCE: 16932.002  
; CURRENT APPLICATION NUMBER: US/10/081,119  
; CURRENT FILING DATE: 2002-02-21  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/289,813  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 821  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-081-119-16

Query Match 96.3%; Score 52; DB 4; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||.|||||  
Db 354 TFCGTLAYVAPE 365

RESULT 12  
US-10-951-389-16  
; Sequence 16, Application US/10951389  
; Publication No. US20050059627A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
; TITLE OF INVENTION: Target in Cancer  
; FILE REFERENCE: 16932.002  
; CURRENT APPLICATION NUMBER: US/10/951,389  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/289,813  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 821  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-951-389-16

Query Match 96.3%; Score 52; DB 5; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||.|||||  
Db 354 TFCGTLAYVAPE 365

RESULT 13  
US-10-951-406-16  
; Sequence 16, Application US/10951406  
; Publication No. US20050059630A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
; TITLE OF INVENTION: Target in Cancer  
; FILE REFERENCE: 16932.002  
; CURRENT APPLICATION NUMBER: US/10/951,406  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/289,813  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 821  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-951-406-16

Query Match 96.3%; Score 52; DB 5; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||.|||||  
Db 354 TFCGTLAYVAPE 365

RESULT 14  
US-10-951-477-16  
; Sequence 16, Application US/10951477

; Publication No. US20050063974A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic  
; TITLE OF INVENTION: Target in Cancer  
; FILE REFERENCE: 16932.002  
; CURRENT APPLICATION NUMBER: US/10/951,477  
; CURRENT FILING DATE: 2004-09-27  
; PRIOR APPLICATION NUMBER: US/10/081,119  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/289,813  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 821  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-951-477-16

Query Match 96.3%; Score 52; DB 5; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 354 TFCGTLAYVAPE 365

RESULT 15  
US-10-977-087-16  
; Sequence 16, Application US/10977087  
; Publication No. US20050130926A1  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; APPLICANT: Chan, Vivien W.  
; APPLICANT: Kaufmann, Joerg  
; APPLICANT: Xin, Hong  
; APPLICANT: Kennedy, Giulia C.  
; APPLICANT: Khoja, Hamiduddin  
; APPLICANT: Shyamala, Venkatakrishna  
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS  
; TITLE OF INVENTION: AND THEIR METHODS OF USE V  
; FILE REFERENCE: 2300-21986  
; CURRENT APPLICATION NUMBER: US/10/977,087  
; CURRENT FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: 10/081,119  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/271,254  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 10/360,848  
; PRIOR FILING DATE: 2003-02-06  
; PRIOR APPLICATION NUMBER: 09/570,593  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: 60/134,112  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 10/763,692  
; PRIOR FILING DATE: 2004-01-22  
; PRIOR APPLICATION NUMBER: 09/626,301  
; PRIOR FILING DATE: 2000-07-25  
; PRIOR APPLICATION NUMBER: 60/148,936  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: 60/145,612  
; PRIOR FILING DATE: 1999-07-26  
; PRIOR APPLICATION NUMBER: 10/698,959  
; PRIOR FILING DATE: 2003-10-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 84  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16

; LENGTH: 821  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-977-087-16

Query Match 96.3%; Score 52; DB 5; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 354 TFCGTLAYVAPE 365

RESULT 16  
US-10-369-493-22067  
; Sequence 22067, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 22067  
; LENGTH: 823  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-10-369-493-22067

Query Match 96.3%; Score 52; DB 4; Length 823;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 569 TFCGTYEYLAPE 580

RESULT 17  
US-09-801-368-312  
; Sequence 312, Application US/09801368  
; Patent No. US20020128250A1  
; GENERAL INFORMATION:  
; APPLICANT: Busby, Robert  
; APPLICANT: Cali, Brian  
; APPLICANT: Hecht, Peter  
; APPLICANT: Holtzman, Doug  
; APPLICANT: Madden, Kevin  
; APPLICANT: Maxon, Mary  
; APPLICANT: Milne, Todd  
; APPLICANT: No. US20020128250A1man, Thea  
; APPLICANT: Royer, John  
; APPLICANT: Salama, Sofie  
; APPLICANT: Sherman, Amir  
; APPLICANT: Silva, Jeff  
; APPLICANT: Summers, Eric  
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
; FILE REFERENCE: 109272.147  
; CURRENT APPLICATION NUMBER: US/09/801,368  
; CURRENT FILING DATE: 2001-03-07  
; PRIOR APPLICATION NUMBER: US 09/487,558  
; PRIOR FILING DATE: 2000-01-19  
; PRIOR APPLICATION NUMBER: US 60/160,587  
; PRIOR FILING DATE: 1999-10-20

; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 312  
; LENGTH: 824  
; TYPE: PRT  
; ORGANISM: Saccharomyces cerevisiae  
US-09-801-368-312

Query Match 96.3%; Score 52; DB 3; Length 824;  
Best Local Similarity 75.0%; Pred. No. 0.38;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 570 TFCGTTEYLAP 581

RESULT 18  
US-10-732-923-10691  
; Sequence 10691, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; PRIOR FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 10691  
; LENGTH: 917  
; TYPE: PRT  
; ORGANISM: Botryotinia fuckeliana  
US-10-732-923-10691

Query Match 96.3%; Score 52; DB 5; Length 917;  
Best Local Similarity 75.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 674 TFCGTTEYLAP 685

RESULT 19  
US-10-732-923-10655  
; Sequence 10655, Application US/10732923  
; Publication No. US20050108791A1  
; GENERAL INFORMATION:  
; APPLICANT: Edgerton, Michael D  
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES  
; FILE REFERENCE: 38-15(52796)C  
; CURRENT APPLICATION NUMBER: US/10/732,923  
; CURRENT FILING DATE: 2003-12-10  
; PRIOR APPLICATION NUMBER: 10/310,154  
; PRIOR FILING DATE: 2002-12-04  
; NUMBER OF SEQ ID NOS: 24149  
; SEQ ID NO 10655  
; LENGTH: 919  
; TYPE: PRT  
; ORGANISM: Aspergillus nidulans  
US-10-732-923-10655

Query Match 96.3%; Score 52; DB 5; Length 919;  
Best Local Similarity 75.0%; Pred. No. 0.42;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 683 TFCGTTEYLAP 694

RESULT 20  
US-10-148-786A-42  
; Sequence 42, Application US/10148786A  
; Publication No. US20030143656A1  
; GENERAL INFORMATION:  
; APPLICANT: Alessi, Dario  
; APPLICANT: Biondi, Riccardo  
; TITLE OF INVENTION: Protein Kinase Regulation  
; FILE REFERENCE: 002.00210  
; CURRENT APPLICATION NUMBER: US/10/148,786A  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-148-786A-42

Query Match 94.4%; Score 51; DB 4; Length 12;  
Best Local Similarity 75.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 1 TFCGTTEYLAP 12

RESULT 21  
US-10-240-315-4  
; Sequence 4, Application US/10240315  
; Publication No. US20030224378A1  
; GENERAL INFORMATION:  
; APPLICANT: PLOWMAN, GREGORY D.  
; APPLICANT: WHYTE, DAVID  
; APPLICANT: MANNING, GERARD  
; APPLICANT: SUDARSANAM, SUCHA  
; APPLICANT: MARTINEZ, RICARDO  
; APPLICANT: CAENEPEEL, SEAN R.  
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE  
; FILE REFERENCE: 038602-1456  
; CURRENT APPLICATION NUMBER: US/10/240,315  
; CURRENT FILING DATE: 2002-10-01  
; PRIOR APPLICATION NUMBER: PCT/US01/11675  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: 60/195,953  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: 60/201,015  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/213,805  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 198  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-240-315-4

Query Match 94.4%; Score 51; DB 4; Length 198;  
Best Local Similarity 75.0%; Pred. No. 0.16;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 75 TFCGTTEYLAP 86

RESULT 22  
US-10-220-955-13  
; Sequence 13, Application US/10220955  
; Publication No. US20030211989A1

```
; GENERAL INFORMATION:
; APPLICANT: BLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602-1401
; CURRENT APPLICATION NUMBER: US/10/220,955
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-220-955-13

Query Match          94.4%; Score 51; DB 4; Length 281;
Best Local Similarity 75.0%; Pred. No. 0.22; 3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
Db      125 TFCGTIEYWAPE 136

RESULT 23
US-10-425-115-222617
; Sequence 222617, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 222617
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_134618C.1.pdp
; US-10-425-115-222617

Query Match          94.4%; Score 51; DB 4; Length 299;
Best Local Similarity 75.0%; Pred. No. 0.23; 3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
Db      181 TFCGTFSYWAPE 192

RESULT 24
US-11-007-819-39
; Sequence 39, Application US/11007819
; Publication No. US20050235377A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Jayaprakash, T.L.
; APPLICANT: Thai, Carolyn J.
; APPLICANT: Narayanan, K.K.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Dotson, Stanton B.
; TITLE OF INVENTION: OsPK7
```

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; FILE REFERENCE: 38-21(53203)B
; CURRENT APPLICATION NUMBER: US/11/007,819
; CURRENT FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Medicago truncatula
; US-11-007-819-39

Query Match          94.4%; Score 51; DB 6; Length 310;
Best Local Similarity 75.0%; Pred. No. 0.24; 3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
Db      184 TFCGTPAYWAPE 195

RESULT 25
US-10-369-493-3875
; Sequence 3875, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3875
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(311)
; OTHER INFORMATION: unsure at all Xaa locations
; US-10-369-493-3875

Query Match          94.4%; Score 51; DB 4; Length 311;
Best Local Similarity 75.0%; Pred. No. 0.24; 3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
Db      210 TFCGTICYSAPE 221

RESULT 26
US-10-217-574-16
; Sequence 16, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT APPLICATION NUMBER: US/10/217,574
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
```

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; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-574-16

Query Match          94.4%; Score 51; DB 4; Length 333;
Best Local Similarity 75.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      168 TFCGTIEYMAPE 179

RESULT 27
US-10-217-555-16
; Sequence 16, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; FILE REFERENCE: 44236
; CURRENT APPLICATION NUMBER: US/10/217,555
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Sequence source
; OTHER INFORMATION: uncertain
US-10-217-555-16

Query Match          94.4%; Score 51; DB 4; Length 333;
Best Local Similarity 75.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      168 TFCGTIEYMAPE 179

RESULT 28
US-10-425-114-54517
; Sequence 54517, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```

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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54517
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4656-028-E10_FLI.pep
US-10-425-114-54517

Query Match          94.4%; Score 51; DB 4; Length 342;
Best Local Similarity 75.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      69 TFCGTIEYMAPE 80

RESULT 29
US-11-007-819-33
; Sequence 33, Application US/11007819
; Publication No. US20050235377A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Jayaprakash, T.L.
; APPLICANT: Thai, Carolyn J.
; APPLICANT: Narayanan, K.K.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Dotson, Stanton B.
; TITLE OF INVENTION: OapK7
; FILE REFERENCE: 38-21(53203)B
; CURRENT APPLICATION NUMBER: US/11/007,819
; CURRENT FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Allium porrum
; OTHER INFORMATION: uncertain
US-11-007-819-33

Query Match          94.4%; Score 51; DB 6; Length 368;
Best Local Similarity 75.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      161 TFCGTPAYVAPE 172

RESULT 30
US-11-007-819-35
; Sequence 35, Application US/11007819
; Publication No. US20050235377A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Jayaprakash, T.L.
; APPLICANT: Thai, Carolyn J.
; APPLICANT: Narayanan, K.K.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Dotson, Stanton B.
; TITLE OF INVENTION: OapK7
; FILE REFERENCE: 38-21(53203)B
; CURRENT APPLICATION NUMBER: US/11/007,819
; CURRENT FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 35
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (248)..(248)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-007-819-35

Query Match          94.4%; Score 51; DB 6; Length 392;
Best Local Similarity 75.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
DB      84 TFCGTPAYVAPE 95

RESULT 31
US-10-425-114-43382
; Sequence 43382, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43382
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700208165_FLI.pep
US-10-425-114-43382

Query Match          94.4%; Score 51; DB 4; Length 403;
Best Local Similarity 75.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
DB      88 TFCGTPAYVAPE 99

RESULT 32
US-10-425-114-43052
; Sequence 43052, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43052
; LENGTH: 427
; TYPE: PRT
```

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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700891395_FLI.pep
US-10-425-114-43052

Query Match          94.4%; Score 51; DB 4; Length 427;
Best Local Similarity 75.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
DB      76 TFCGTPAYVAPE 87

RESULT 33
US-10-425-114-40884
; Sequence 40884, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40884
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700870679_FLI.pep
US-10-425-114-40884

Query Match          94.4%; Score 51; DB 4; Length 439;
Best Local Similarity 75.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
DB      199 TFCGTPAYVAPE 210

RESULT 34
US-09-740-627-10
; Sequence 10, Application US/09740627
; Patent No. US20020012964A1
; GENERAL INFORMATION:
; APPLICANT: Nakanishi, Makoto
; TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
; FILE REFERENCE: 06501-071001
; CURRENT APPLICATION NUMBER: US/09/740,627
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/JP99/03350
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: JP 10/192467
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-09-740-627-10

Query Match          94.4%; Score 51; DB 3; Length 460;
Best Local Similarity 75.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 TFCGTXYYXAPE 13  
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Db 328 TFCGTMGYLAPE 339

RESULT 35  
US-10-369-493-12994  
; Sequence 12994, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 12994  
; LENGTH: 464  
; TYPE: PRT  
; ORGANISM: Aspergillus nidulans  
; NAME/KEY: unsure  
; LOCATION: (1)..(464)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-10-369-493-12994

Query Match 94.4%; Score 51; DB 4; Length 464;  
Best Local Similarity 75.0%; Pred. No. 0.34; Mismatches 0; Indels 3; Gaps 0;  
Matches 9; Conservative 0;

QY 2 TFCGTXYYXAPE 13  
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Db 190 TFCGTVCYSAPE 201

RESULT 36  
US-10-425-114-57769  
; Sequence 57769, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 57769  
; LENGTH: 469  
; TYPE: PRT  
; ORGANISM: Glycine max  
; NAME/KEY: misc feature  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY081D01\_FLI.pap  
US-10-425-114-57769

Query Match 94.4%; Score 51; DB 4; Length 469;  
Best Local Similarity 75.0%; Pred. No. 0.35; Mismatches 0; Indels 3; Gaps 0;  
Matches 9; Conservative 0;

QY 2 TFCGTXYYXAPE 13

Db 146 TFCGTPAYVAPE 157

RESULT 37  
US-10-424-599-269103  
; Sequence 269103, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 269103  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Glycine max  
; NAME/KEY: unsure  
; LOCATION: (1)..(475)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_85020C.1.pap  
US-10-424-599-269103

Query Match 94.4%; Score 51; DB 4; Length 475;  
Best Local Similarity 75.0%; Pred. No. 0.35; Mismatches 0; Indels 3; Gaps 0;  
Matches 9; Conservative 0;

QY 2 TFCGTXYYXAPE 13  
||||| |  
Db 152 TFCGTPAYVAPE 163

RESULT 38  
US-11-007-819-20  
; Sequence 20, Application US/11007819  
; Publication No. US20050235377A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology LLC  
; APPLICANT: Dasgupta, Santanu  
; APPLICANT: Javaprakash, T.L.  
; APPLICANT: Thai, Carolyn J.  
; APPLICANT: Narayanan, K.K.  
; APPLICANT: Ruff, Thomas G.  
; APPLICANT: Dotson, Stanton B.  
; TITLE OF INVENTION: OapK7  
; FILE REFERENCE: 38-21(53203)B  
; CURRENT APPLICATION NUMBER: US/11/007,819  
; CURRENT FILING DATE: 2004-12-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Glycine max  
; NAME/KEY: misc feature  
; LOCATION: (6)..(6)  
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-11-007-819-20

Query Match 94.4%; Score 51; DB 6; Length 475;  
Best Local Similarity 75.0%; Pred. No. 0.35; Mismatches 0; Indels 3; Gaps 0;  
Matches 9; Conservative 0;

QY 2 TFCGTXYYXAPE 13



Db 152 TFCGTPAYVAPE 163

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RESULT 39
US-11-007-819-43
; Sequence 43, Application US/11007819
; Publication No. US20050235377A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Jayaprakash, T.L.
; APPLICANT: Thai, Carolyn J.
; APPLICANT: Narayanan, K.K.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Dotson, Stanton B.
; TITLE OF INVENTION: Oepk7
; FILE REFERENCE: 38-21(53203)B
; CURRENT APPLICATION NUMBER: US/11/007,819
; CURRENT FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-007-819-43

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Query Match 94.4%; Score 51; DB 6; Length 483;  
 Best Local Similarity 75.0%; Pred. No. 0.36;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 Db 186 TFCGTPAYVAPE 197

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RESULT 40
US-11-007-819-8
; Sequence 8, Application US/11007819
; Publication No. US20050235377A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Dasgupta, Santanu
; APPLICANT: Jayaprakash, T.L.
; APPLICANT: Thai, Carolyn J.
; APPLICANT: Narayanan, K.K.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Dotson, Stanton B.
; TITLE OF INVENTION: Oepk7
; FILE REFERENCE: 38-21(53203)B
; CURRENT APPLICATION NUMBER: US/11/007,819
; CURRENT FILING DATE: 2004-12-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Zea mays
US-11-007-819-8

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Query Match 94.4%; Score 51; DB 6; Length 489;  
 Best Local Similarity 75.0%; Pred. No. 0.36;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
 Db 179 TFCGTPAYVAPE 190

Search completed: February 18, 2006, 08:21:13  
 Job time : 160.421 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2006, 08:17:29 ; Search time 14.3684 Seconds  
(without alignments)  
12.861 Million cell updates/sec

Title: US-09-868-131C-48  
Perfect score: 54  
Sequence: 1 XTFCGTXXYAPE 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA New.\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
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- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	94.4	495	6	US-10-770-726-81
2	50	92.6	39	7	US-11-192-341-3
3	50	92.6	351	7	US-11-099-958-2
4	50	92.6	480	7	US-11-109-156-18
5	50	92.6	543	6	US-10-821-234-1158
6	50	92.6	705	6	US-10-995-561-856
7	50	92.6	706	6	US-10-995-561-855
8	50	92.6	706	7	US-10-099-958-1
9	50	92.6	737	7	US-11-152-366-28
10	48	88.9	367	7	US-11-151-601-2
11	47	87.0	740	6	US-10-878-556A-129
12	46	85.2	713	6	US-10-995-561-881
13	46	85.2	729	6	US-10-995-561-878
14	46	85.2	737	6	US-10-995-561-880
15	46	85.2	744	6	US-10-995-561-876
16	46	85.2	752	6	US-10-995-561-879
17	46	85.2	753	6	US-10-995-561-877
18	46	85.2	742	6	US-10-770-726-76
19	46	85.2	942	6	US-10-329-258-16
20	44	81.5	321	7	US-11-072-512-2467
21	44	81.5	341	7	US-11-092-168-4
22	44	81.5	343	7	US-11-092-168-3
23	44	81.5	350	6	US-10-497-767-4
24	44	81.5	351	7	US-11-132-142-13
25	44	81.5	351	7	US-11-132-142-14

353	7	US-11-132-142-11	Sequence 11, Appl
381	7	US-11-132-142-9	Sequence 9, Appl
395	7	US-11-132-142-12	Sequence 12, Appl
398	7	US-11-132-142-7	Sequence 7, Appl
462	7	US-11-132-142-10	Sequence 10, Appl
480	7	US-11-132-142-6	Sequence 6, Appl
515	7	US-11-132-142-8	Sequence 8, Appl
548	7	US-11-132-142-5	Sequence 5, Appl
603	6	US-10-770-726-75	Sequence 75, Appl
631	7	US-11-241-056-11	Sequence 11, Appl
766	7	US-11-151-601-8	Sequence 8, Appl
30	7	US-11-106-932-41	Sequence 41, Appl
332	6	US-10-497-767-3	Sequence 3, Appl
355	7	US-11-241-056-10	Sequence 10, Appl
473	7	US-11-152-366-34	Sequence 34, Appl
651	6	US-10-770-726-67	Sequence 67, Appl
651	7	US-11-177-138-10	Sequence 10, Appl
685	7	US-11-169-041-194	Sequence 194, Appl
970	6	US-10-770-726-86	Sequence 86, Appl
231	7	US-11-151-601-5	Sequence 5, Appl
231	7	US-11-151-601-12	Sequence 12, Appl
256	6	US-10-877-346-72	Sequence 72, Appl
256	6	US-10-877-346-74	Sequence 74, Appl
256	6	US-10-877-346-74	Sequence 183, Appl
275	6	US-10-523-477-10	Sequence 10, Appl
344	6	US-10-770-726-84	Sequence 84, Appl
344	7	US-11-109-156-13	Sequence 13, Appl
344	7	US-11-092-168-2	Sequence 2, Appl
403	6	US-10-523-477-11	Sequence 11, Appl
403	6	US-10-770-726-83	Sequence 83, Appl
403	6	US-10-770-726-85	Sequence 85, Appl
403	7	US-11-109-156-12	Sequence 12, Appl
403	7	US-11-092-168-1	Sequence 1, Appl
1133	6	US-10-821-234-1219	Sequence 1219, Ap
317	7	US-11-137-315A-4	Sequence 4, Appl
359	7	US-11-089-425A-4	Sequence 4, Appl
409	7	US-11-137-315A-6	Sequence 6, Appl
448	7	US-11-089-425A-1	Sequence 1, Appl
476	6	US-10-770-726-56	Sequence 56, Appl
501	7	US-11-124-368A-34	Sequence 324, Appl
514	7	US-11-125-295-2	Sequence 2, Appl
514	7	US-11-072-512-3509	Sequence 3509, Ap
714	7	US-11-121-419-2	Sequence 2, Appl
714	7	US-11-121-419-17	Sequence 17, Appl
322	6	US-10-055-877-26	Sequence 26, Appl
374	6	US-10-055-877-20	Sequence 20, Appl
374	6	US-10-055-877-22	Sequence 22, Appl
374	7	US-11-037-243-61	Sequence 61, Appl
400	7	US-11-111-239-12	Sequence 12, Appl
465	7	US-11-152-366-33	Sequence 33, Appl
445	6	US-10-770-726-70	Sequence 70, Appl
745	6	US-10-995-561-659	Sequence 659, Appl
745	7	US-11-109-156-14	Sequence 14, Appl
756	7	US-11-222-158-2	Sequence 2, Appl
23	7	US-11-066-967-96	Sequence 96, Appl
28	7	US-11-066-967-99	Sequence 99, Appl
225	7	US-11-125-295-5	Sequence 5, Appl
236	7	US-11-125-295-7	Sequence 7, Appl
266	7	US-11-241-056-13	Sequence 13, Appl
375	7	US-11-241-056-8	Sequence 8, Appl
393	7	US-11-111-239-11	Sequence 11, Appl
396	7	US-11-125-295-11	Sequence 11, Appl
407	7	US-11-125-295-9	Sequence 9, Appl
431	7	US-11-152-366-29	Sequence 29, Appl
443	7	US-11-152-366-30	Sequence 30, Appl
1360	7	US-11-241-056-14	Sequence 14, Appl
16	7	US-11-066-967-88	Sequence 88, Appl
16	7	US-11-066-967-93	Sequence 93, Appl
18	7	US-11-066-967-100	Sequence 100, Appl
18	7	US-11-066-967-104	Sequence 104, Appl
327	7	US-11-072-512-3184	Sequence 3184, Ap

Sequence 87, Appl  
Sequence 1137, Ap

99 34 63.0 547 6 US-10-770-726-87  
100 34 63.0 588 6 US-10-821-234-1137

## ALIGNMENTS

RESULT 1  
US-10-770-726-81  
; Sequence 81, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 81  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-770-726-81

Query Match 94.4%; Score 51; DB 6; Length 495;  
Best Local Similarity 75.0%; Pred. No. 0.012;  
Matches 9; Conservative 0; Mismatches 0; Gaps 0;  
Indels 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 241 TFCGTIEYWAPE 252

RESULT 2  
US-11-192-341-3  
; Sequence 3, Application US/11192341  
; Publication No. US20060030583A1  
; GENERAL INFORMATION:  
; APPLICANT: SGX Pharmaceuticals, Inc.  
; APPLICANT: Arnold, William D.  
; APPLICANT: Bonnaud, Pierre  
; APPLICANT: Gosberg, Andreas  
; APPLICANT: Li, Zhe  
; APPLICANT: McDonald, Ian  
; APPLICANT: Steensma, Ruw W.  
; APPLICANT: Wilson, Mark E.  
; TITLE OF INVENTION: Pyrrolo-Pyridine Kinase Modulators  
; FILE REFERENCE: 022132-004510US  
; CURRENT APPLICATION NUMBER: US/11/192,341  
; CURRENT FILING DATE: 2005-07-27  
; PRIOR APPLICATION NUMBER: 60/683,510  
; PRIOR FILING DATE: 2003-05-19  
; PRIOR APPLICATION NUMBER: 60/591,888  
; PRIOR FILING DATE: 2004-07-27  
; PRIOR APPLICATION NUMBER: 60/591,887  
; PRIOR FILING DATE: 2004-07-27  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct - PDKtide peptide substrate  
US-11-192-341-3

Query Match 92.6%; Score 50; DB 7; Length 39;  
Best Local Similarity 75.0%; Pred. No. 0.0022;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
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DB 2 TFCGTPEYLAPE 13

RESULT 3  
US-11-099-958-2  
; Sequence 2, Application US/11099958  
; Publication No. US20060003431A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Zhang Bao  
; APPLICANT: Olland, Stephane  
; APPLICANT: Wolfgram, Scott  
; APPLICANT: Malakian, Karl  
; APPLICANT: Lin, Laura  
; APPLICANT: Stahl, Mark  
; APPLICANT: Lee, Julie  
; APPLICANT: Fitz, Lori  
; APPLICANT: Greco, Rita  
; APPLICANT: Chaudhary, Divya  
; APPLICANT: Somers, William Stuart  
; APPLICANT: Mosyak, Lidia  
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA  
; FILE REFERENCE: 16163-018001  
; CURRENT APPLICATION NUMBER: US/11/099,958  
; CURRENT FILING DATE: 2005-04-06  
; PRIOR APPLICATION NUMBER: US 60/560,441  
; PRIOR FILING DATE: 2004-04-07  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 351  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-099-958-2

Query Match 92.6%; Score 50; DB 7; Length 351;  
Best Local Similarity 75.0%; Pred. No. 0.014;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
DB 177 TFCGTPDYIAPE 188

RESULT 4  
US-11-109-156-18  
; Sequence 18, Application US/11109156  
; Publication No. US20050250144A1  
; GENERAL INFORMATION:  
; APPLICANT: Toshio Ota  
; APPLICANT: Takao Isogai  
; APPLICANT: Tetsuo Nishikawa  
; APPLICANT: Koji Hayashi  
; APPLICANT: Kaoru Otsuka  
; APPLICANT: Jun-ichi Yamamoto  
; APPLICANT: Shizuko Ishii  
; APPLICANT: Tomoyasu Sugiyama  
; APPLICANT: Ai Wakamatsu  
; APPLICANT: Keiichi Nagai  
; APPLICANT: Tetsuji Otsuki  
; APPLICANT: Shin-ichi Funahashi  
; APPLICANT: Chiaki Senoo  
; APPLICANT: Jun-ichi Nezu  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN  
; TITLE OF INVENTION: PHOSPHATASE  
; FILE REFERENCE: 06501-099002  
; CURRENT APPLICATION NUMBER: US/11/109,156  
; CURRENT FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: US/10/060,065  
; PRIOR FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP00/05061  
US-11-109-156-18

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; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 60/183,322
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: JP 11-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-109-156-18

Query Match          92.6%; Score 50; DB 7; Length 480;
Best Local Similarity 75.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY      2 TFCGTXYYXAPE 13
      ||||| | |||
Db      308 TFCGTPPEYLAPE 319

RESULT 5
US-10-821-234-1158
; Sequence 1158, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarjani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1158
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1158

Query Match          92.6%; Score 50; DB 6; Length 543;
Best Local Similarity 75.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY      2 TFCGTXYYXAPE 13
      ||||| | |||
Db      368 TFCGTPPEYLAPE 379

RESULT 6
US-10-995-561-856
; Sequence 856, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561

; PRIOR FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 856
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-856

Query Match          92.6%; Score 50; DB 6; Length 705;
Best Local Similarity 75.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXYYXAPE 13
      ||||| | |||
Db      537 TFCGTPDYIAPE 548

RESULT 7
US-10-995-561-855
; Sequence 855, Application US/10995561
; Publication No. US2005027054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 855
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-855

Query Match          92.6%; Score 50; DB 6; Length 706;
Best Local Similarity 75.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 TFCGTXYYXAPE 13
      ||||| | |||
Db      538 TFCGTPDYIAPE 549

RESULT 8
US-11-099-958-1
; Sequence 1, Application US/11099958
; Publication No. US20060003431A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Zhang Bao
; APPLICANT: Olland, Stephane
; APPLICANT: Wolfrom, Scott
; APPLICANT: Malakian, Karl
; APPLICANT: Lin, Laura
; APPLICANT: Stahl, Mark
; APPLICANT: Lee, Julie
; APPLICANT: Fitz, Lori
; APPLICANT: Greco, Rita
; APPLICANT: Chaudhary, Divya
; APPLICANT: Somers, William Stuart
; APPLICANT: Mosyak, Lidia
; TITLE OF INVENTION: STRUCTURE OF PROTEIN KINASE C THETA
; FILE REFERENCE: 16163-018001
; CURRENT APPLICATION NUMBER: US/11/099,958
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US 60/560,441
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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; LENGTH: 706
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-099-958-1

Query Match          92.6%; Score 50; DB 7; Length 706;
Best Local Similarity 75.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
    ||||| |||||
Db 538 TFCGTPDYIAPE 549

RESULT 9
US-11-152-366-28
; Sequence 28, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-28

Query Match          92.6%; Score 50; DB 7; Length 737;
Best Local Similarity 75.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
    ||||| |||||
Db 566 TFCGTPDYIAPE 577

RESULT 10
US-11-151-601-2
; Sequence 2, Application US/11151601
; Publication No. US20060003413A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; TITLE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: MPI00-054P1CPI0KNIDVIM
; CURRENT APPLICATION NUMBER: US/11/151,601
; CURRENT FILING DATE: 2005-06-13
; PRIOR APPLICATION NUMBER: US 10/170,789
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
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; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-151-601-2

Query Match          88.9%; Score 48; DB 7; Length 367;
Best Local Similarity 66.7%; Pred. No. 0.034;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
    ||||| |||||
Db 174 TFCGSPAYAAPE 185

RESULT 11
US-10-878-556A-129
; Sequence 129, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-08-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/k6a3_human
; DATABASE ENTRY DATE: 1996-10-01
US-10-878-556A-129

Query Match          87.0%; Score 47; DB 6; Length 740;
Best Local Similarity 66.7%; Pred. No. 0.095;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
    ||||| |||||
Db 227 SFCGIVEYWAPE 238

RESULT 12
US-10-995-561-881
; Sequence 881, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 881
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; LENGTH: 713
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-881

Query Match      85.2%; Score 46; DB 6; Length 713;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
   ||||: ||||
Db 211 TFCGSPPYAAPE 222

RESULT 13
US-10-995-561-878
; Sequence 878, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 878
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-878

Query Match      85.2%; Score 46; DB 6; Length 729;
Best Local Similarity 66.7%; Pred. No. 0.14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
   ||||: ||||
Db 211 TFCGSPPYAAPE 222

RESULT 14
US-10-995-561-880
; Sequence 880, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 880
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-880

Query Match      85.2%; Score 46; DB 6; Length 737;
Best Local Similarity 66.7%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
   ||||: ||||
Db 211 TFCGSPPYAAPE 222

RESULT 15
US-10-995-561-879
; Sequence 879, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 879
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-879

Query Match      85.2%; Score 46; DB 6; Length 752;
Best Local Similarity 66.7%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13
   ||||: ||||
Db 234 TFCGSPPYAAPE 245

RESULT 17
US-10-995-561-877
; Sequence 877, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 877
; LENGTH: 753
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-877

Query Match      85.2%; Score 46; DB 6; Length 753;
Best Local Similarity 66.7%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||: |||||
Db      211 TFCGSPPYAAPE 222

RESULT 18
US-10-770-726-76
; Sequence 76, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-76

Query Match      85.2%; Score 46; DB 6; Length 942;
Best Local Similarity 66.7%; Pred. No. 0.18;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||: |||||
Db      774 TFCGTPFLAPE 785

RESULT 19
US-10-329-258-16
; Sequence 16, Application US/10329258
; Publication No. US2006002423A1
; GENERAL INFORMATION:
; APPLICANT: MUELLER, SABINE
; APPLICANT: GONZALEZ-ZULUETA, MIRELLA
; APPLICANT: FOEHR, ERIK
; APPLICANT: CHIN, DANIEL J.
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION OF
; FILE REFERENCE: AGYT-008US2
; CURRENT APPLICATION NUMBER: US/10/329,258
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/343,422
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 942
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-329-258-16

Query Match      85.2%; Score 46; DB 6; Length 942;
Best Local Similarity 66.7%; Pred. No. 0.18;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||: |||||
Db      774 TFCGTPFLAPE 785
```

```

RESULT 20
US-11-072-512-2467
; Sequence 2467, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cdna
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2467
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2467

Query Match      81.5%; Score 44; DB 7; Length 321;
Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||: |||||
Db      168 TFCGTPFLAPE 179

RESULT 21
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bearss, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
```



```
; US 60/608,529 ;
; US 60/511,486 ;
; US 60/511,489 ;
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4

Query Match      81.5%; Score 44; DB 7; Length 341;
Best Local Similarity 66.7%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAP 13
Db      188 TLGGTPEYLAPE 199

RESULT 22
US-11-092-168-3
; Sequence 3, Application US/11092168
; Publication No. US2005027658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Montigen Pharmaceuticals, Inc.
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bears, David J.
; APPLICANT: Vankavalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-092-168-3

Query Match      81.5%; Score 44; DB 7; Length 343;
Best Local Similarity 66.7%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAP 13
Db      190 TLGGTPEYLAPE 201

RESULT 23
US-10-497-767-4
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```
; Sequence 4, Application US/10497767
; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVORKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VPI/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (10)
; OTHER INFORMATION: Variable amino acid
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (338)
; OTHER INFORMATION: Variable amino acid
; US-10-497-767-4

Query Match      81.5%; Score 44; DB 6; Length 350;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAP 13
Db      197 TLGGTPEYLAPE 208

RESULT 24
US-11-132-142-13
; Sequence 13, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; TITLE OF INVENTION: CYCLIC-AMP-DEPENDENT KINASE AND A TARGET FOR SARS THERAPY
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-11-132-142-13

Query Match      81.5%; Score 44; DB 7; Length 351;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAP 13
Db      198 TLGGTPEYLAPE 209

RESULT 25
US-11-132-142-14
```

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; Sequence 14, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-142-14

Query Match      81.5%; Score 44; DB 7; Length 351;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
DB      198 TLCGTPEYLAPE 209

RESULT 26
US-11-132-142-11
; Sequence 11, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Anopheles sp.
US-11-132-142-11

Query Match      81.5%; Score 44; DB 7; Length 353;
Best Local Similarity 66.7%; Pred. No. 0.19;
Matches 8; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
DB      200 TLCGTPEYLAPE 211

RESULT 27
US-11-132-142-9
; Sequence 9, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9

Query Match      81.5%; Score 44; DB 7; Length 381;
Best Local Similarity 66.7%; Pred. No. 0.2;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
DB      226 TLCGTPEYLAPE 237

RESULT 28
US-11-132-142-12
; Sequence 12, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Danio
US-11-132-142-12

Query Match      81.5%; Score 44; DB 7; Length 395;
Best Local Similarity 66.7%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
DB      242 TLCGTPEYLAPE 253

RESULT 29
US-11-132-142-7
; Sequence 7, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Leishmania sp.
US-11-132-142-9
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; ORGANISM: Saccharomyces sp.
US-11-132-142-7

Query Match      81.5%; Score 44; DB 7; Length 398;
Best Local Similarity 66.7%; Pred. No. 0.21;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      242 TLGTPDYIAPE 253

RESULT 30
US-11-132-142-10
; Sequence 10, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Amblyomma
US-11-132-142-10

Query Match      81.5%; Score 44; DB 7; Length 462;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      309 TLGTPDYIAPE 320

RESULT 31
US-11-132-142-6
; Sequence 6, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Aspergillus sp.
US-11-132-142-6

Query Match      81.5%; Score 44; DB 7; Length 480;
Best Local Similarity 66.7%; Pred. No. 0.24;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      430 TLGTPDYIAPE 441

RESULT 34
US-10-770-726-75
; Sequence 75, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

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Db      323 TLGTPDYIAPE 334

RESULT 32
US-11-132-142-8
; Sequence 8, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Cryptococcus sp.
US-11-132-142-8

Query Match      81.5%; Score 44; DB 7; Length 515;
Best Local Similarity 66.7%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      357 TLGTPDYIAPE 368

RESULT 33
US-11-132-142-5
; Sequence 5, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Caenorhabditis sp.
US-11-132-142-5

Query Match      81.5%; Score 44; DB 7; Length 548;
Best Local Similarity 66.7%; Pred. No. 0.27;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXYXAPE 13
      |||||
Db      430 TLGTPDYIAPE 441

RESULT 34
US-10-770-726-75
; Sequence 75, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
```

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; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-75

Query Match      81.5%; Score 44; DB 6; Length 603;
Best Local Similarity 66.7%; Pred. No. 0.29;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 TFCGTXXYXKPE 13
Db 210 TLCGTPNYIAPE 221

RESULT 35
US-11-241-056-11
; Sequence 11, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-241-056-11

Query Match      81.5%; Score 44; DB 7; Length 631;
Best Local Similarity 58.3%; Pred. No. 0.31;
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

QY 2 TFCGTXXYXKPE 13
Db 212 TFCGSPLYASPE 223

RESULT 36
US-11-151-601-8
; Sequence 8, Application US/11151601
; Publication No. US20060003413A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; FILE REFERENCE: MPI00-054PIRC10WNI01M
; CURRENT APPLICATION NUMBER: US/11/151,601
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; CURRENT FILING DATE: 2005-06-13
; PRIOR APPLICATION NUMBER: US 10/170,789
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-151-601-8

Query Match      81.5%; Score 44; DB 7; Length 766;
Best Local Similarity 66.7%; Pred. No. 0.36;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 TFCGTXXYXKPE 13
Db 550 TVCGPTTYVAPE 561

RESULT 37
US-11-106-932-41
; Sequence 41, Application US/11106932
; Publication No. US20050260897A1
; GENERAL INFORMATION:
; APPLICANT: WANG, KA-WANG KEVIN
; APPLICANT: HAYES, RONALD
; APPLICANT: LIU, MING CHEN
; APPLICANT: OLI, MONIKA
; TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
; FILE REFERENCE: 5853-549-1
; CURRENT APPLICATION NUMBER: US/11/106,932
; CURRENT FILING DATE: 2005-04-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-932-41

Query Match      77.8%; Score 42; DB 7; Length 30;
Best Local Similarity 66.7%; Pred. No. 0.058;
Matches 8; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 TFCGTXXYXKPE 13
Db 12 TVCGTPGYCAPE 23

RESULT 38
US-10-497-767-3
; Sequence 3, Application US/10497767
```

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; Publication No. US20050261836A1
; GENERAL INFORMATION:
; APPLICANT: VERTEX PHARMACEUTICALS INCORPORATED
; APPLICANT: MENG, WUYI
; APPLICANT: SWENSON, LOVOKA
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF MITOGEN-ACTIVATED PROTEIN
; TITLE OF INVENTION: KINASE-ACTIVATED PROTEIN KINASE 2 AND BINDING POCKETS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: VP1/01-13 PCT
; CURRENT APPLICATION NUMBER: US/10/497,767
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/337,513
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-497-767-3

Query Match          77.8%; Score 42; DB 6; Length 332;
Best Local Similarity 66.7%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAPE 13
DB      177 TAGCTPGYVAPE 188

RESULT 39
US-11-241-056-10
; Sequence 10, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241,056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-241-056-10

Query Match          77.8%; Score 42; DB 7; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.45;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAPE 13
DB      180 TAGCTPGYVAPE 191

RESULT 40
US-11-152-366-34
; Sequence 34, Application US/11152366
; Publication No. US20060014184A1
; GENERAL INFORMATION:
; APPLICANT: Brys, Reginald
; APPLICANT: Vandeghinste, Nick
; APPLICANT: Tomme, Peter H. M.
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
```

```
; FILE REFERENCE: P27,880-A USA
; CURRENT APPLICATION NUMBER: US/11/152,366
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/579,307
; PRIOR FILING DATE: 2004-06-14
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-366-34

Query Match          77.8%; Score 42; DB 7; Length 473;
Best Local Similarity 66.7%; Pred. No. 0.57;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TFCGTXXXYXAPE 13
DB      200 TVCGTPGYCAPE 211

Search completed: February 18, 2006, 08:21:40
Job time : 15.3684 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2006, 07:56:34 ; Search time 31.4737 Seconds  
(without alignments)  
39.742 Million cell updates/sec

Title: US-09-868-131C-48

Perfect score: 54

Sequence: 1 XTFCGTXXYAPE 13

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 80:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	96.3	527	2 A53467	protein kinase SNF
2	52	96.3	581	2 T29830	hypothetical prote
3	52	96.3	646	2 T38171	probable serine/th
4	52	96.3	696	2 S55694	protein kinase (EC
5	52	96.3	821	1 A39616	protein kinase RAD
6	52	96.3	823	2 S48986	probable protein k
7	51	94.4	69	2 T07875	protein kinase hom
8	51	94.4	69	2 T07876	protein kinase hom
9	51	94.4	69	2 T07878	protein kinase hom
10	51	94.4	221	2 S20964	ribosomal protein
11	51	94.4	460	2 S58882	protein kinase Cds
12	51	94.4	481	2 JE0377	p70 S6 kinase (EC
13	51	94.4	489	2 T04862	probable serine/th
14	51	94.4	502	2 T02306	probable protein k
15	51	94.4	520	2 G86414	probable protein k
16	51	94.4	525	1 A41687	ribosomal protein
17	51	94.4	525	1 S12906	probable ribosomal
18	51	94.4	525	1 TVRTK6	ribosomal protein
19	51	94.4	580	2 T31529	hypothetical prote
20	51	94.4	674	1 KIMS29	protein kinase C (
21	51	94.4	707	1 A53530	protein kinase C (
22	51	94.4	780	2 T16579	hypothetical prote
23	50	92.6	334	2 A60543	protein kinase (EC
24	50	92.6	422	2 T26334	hypothetical prote
25	50	92.6	431	2 T11854	protein kinase (EC
26	50	92.6	431	2 A48094	serum and glucocor
27	50	92.6	454	1 JC4345	protein kinase (EC
28	50	92.6	462	1 T17287	protein kinase (EC
29	50	92.6	479	1 A59380	protein kinase (EC

30	50	92.6	479	2 A38578	protein kinase 2 (
31	50	92.6	480	1 A39360	protein kinase (EC
32	50	92.6	480	1 JC2437	protein kinase (EC
33	50	92.6	480	1 S33364	protein kinase (EC
34	50	92.6	480	1 S62117	protein kinase (EC
35	50	92.6	481	1 A46288	protein kinase (EC
36	50	92.6	481	1 JC2438	protein kinase (EC
37	50	92.6	483	1 T43234	protein kinase (EC
38	50	92.6	528	1 T21523	protein kinase (EC
39	50	92.6	541	1 T43232	protein kinase (EC
40	50	92.6	546	1 T43233	protein kinase (EC
41	50	92.6	547	2 T22856	hypothetical prote
42	50	92.6	569	2 T50414	probable prolifera
43	50	92.6	586	2 A53758	protein kinase C (
44	50	92.6	587	2 A49509	protein kinase C (
45	50	92.6	592	1 A30314	protein kinase C (
46	50	92.6	592	2 JC1480	protein kinase C (
47	50	92.6	592	2 JN0877	protein kinase C (
48	50	92.6	597	2 T16006	protein kinase C3
49	50	92.6	611	1 A55888	protein kinase (EC
50	50	92.6	634	1 B32392	protein kinase C (
51	50	92.6	639	2 A32545	protein kinase C (
52	50	92.6	671	1 KIHUC1	protein kinase C (
53	50	92.6	671	1 KIRBC1	protein kinase C (
54	50	92.6	671	1 KIRTC1	protein kinase C (
55	50	92.6	671	1 OKBOG	protein kinase (EC
56	50	92.6	672	1 KIBOC	protein kinase C (
57	50	92.6	672	1 KIHUCA	protein kinase C (
58	50	92.6	672	1 KIMS29	protein kinase C (
59	50	92.6	672	1 KIRBC	protein kinase C (
60	50	92.6	672	1 KIRTC	protein kinase C (
61	50	92.6	673	1 KIRTC2	protein kinase C (
62	50	92.6	673	1 KIBOC2	protein kinase C (
63	50	92.6	673	1 KIHUC2	protein kinase C (
64	50	92.6	673	1 KIRBC2	protein kinase C (
65	50	92.6	673	1 KIRTC2	protein kinase C (
66	50	92.6	673	2 S11213	protein kinase C (
67	50	92.6	676	1 S35704	protein kinase C (
68	50	92.6	676	2 A37237	protein kinase C (
69	50	92.6	677	2 JS0178	protein kinase YKR
70	50	92.6	680	2 S37955	protein kinase YPK
71	50	92.6	682	1 KIBOGC	protein kinase C (
72	50	92.6	682	1 A39666	protein kinase C (
73	50	92.6	683	1 A21690	protein kinase (EC
74	50	92.6	683	1 S23478	protein kinase C (
75	50	92.6	686	1 S05702	protein kinase (EC
76	50	92.6	697	1 KIRBGC	protein kinase C (
77	50	92.6	697	1 KIRTCG	protein kinase C (
78	50	92.6	697	2 D24664	protein kinase C (
79	50	92.6	697	2 JN0548	protein kinase C (
80	50	92.6	700	2 A32392	protein kinase C (
81	50	92.6	706	1 A45416	protein kinase C (
82	50	92.6	707	1 A44500	protein kinase C (
83	50	92.6	736	1 KIRBCE	protein kinase C (
84	50	92.6	737	1 KIMSCE	protein kinase C (
85	50	92.6	737	1 KIRTC	protein kinase C (
86	50	92.6	737	1 S28942	protein kinase C (
87	50	92.6	762	1 A46590	protein kinase (EC
88	50	92.6	762	2 S68217	protein kinase (EC
89	50	92.6	762	2 I59329	gag-akt polyprotei
90	50	92.6	763	1 A40831	protein kinase (EC
91	50	92.6	768	1 A34106	protein kinase C h
92	50	92.6	861	2 T15903	protein kinase (EC
93	50	92.6	934	2 T08418	protein kinase (EC
94	50	92.6	1088	2 B34106	protein kinase (EC
95	49	90.7	367	2 T26093	hypothetical prote
96	48	88.9	331	2 T26714	hypothetical prote
97	48	88.9	367	2 T33119	hypothetical prote
98	48	88.9	1363	2 T15653	hypothetical prote
99	47	87.0	521	2 D88640	protein F55A8.2 [l
100	47	87.0	567	2 T33400	protein kinase C h

## ALIGNMENTS

```

RESULT 1
A53467
protein kinase SNF1 homolog wpk4-p58 - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A53467
R:Sano, H.; Yousefian, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 2582-2586, 1994
A:Title: Light and nutritional regulation of transcripts encoding a wheat protein kinase
A:Reference number: A53467; MUID:94195786; PMID:8146158
A:Contents: Kitakami
A:Accession: A53467
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-527 <SAN>
A:Cross-references: UNIPROT:Q41592; UNIPARC:UPI000017A46F; GB:D21204; NID:9487923; PID:9487923
A:Note: sequence extracted from NCBI backbone (NCBIN:146088, NCBIP:146089)
C:Keywords: ATP
F:44-297/Domain: protein kinase ATP-binding motif
F:52-60/Region: protein kinase ATP-binding motif

Query Match 96.3%; Score 52; DB 2; Length 527;
Best Local Similarity 75.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXPAE 13
| | | | | | | | |
Db 202 TFCGTRAYVAPE 213

RESULT 2
T29830
hypothetical protein C09G4.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Nov-2003
C:Accession: T29830
R:Miller, N.; Gattung, S.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C09G4.
A:Reference number: Z20695
A:Accession: T29830
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-581 <MIL>
A:Cross-references: UNIPARC:UPI000017B760; EMBL:U42438; PIDN:AAA83503.1; CESP:C09G4.2
C:Genetics:
A:Gene: CESP:C09G4.2
A:Introns: 22/2; 78/1; 116/1; 195/3; 220/2; 261/2; 335/2; 365/2; 467/2; 493/2
C:Superfamily: cGMP-dependent protein kinase; cAMP receptor protein cyclic nucleotide-bi

Query Match 96.3%; Score 52; DB 2; Length 581;
Best Local Similarity 75.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXPAE 13
| | | | | | | | |
Db 429 TFCGTAEYVAPE 440

RESULT 3
T38171
probable serine/threonine-specific protein kinase (EC 2.7.1.1) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C:Accession: T38171
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z21775
A:Accession: T38171
A:Status: preliminary; translated from GB/EMBL/DBDJ

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A:Molecule type: DNA
A:Residues: 1-646 <DEV>
A:Cross-references: UNIPROT:Q10364; UNIPARC:UPI000012DD14; EMBL:Z70043; NID:gl2020275; PID:gl2020275
A:Experimental source: strain 972h-; cosmid c22E12
C:Genetics:
A:Gene: SPDB:SPAC22E12.14C
A:Map position: 1
C:Keywords: phosphotransferase; protein kinase

Query Match 96.3%; Score 52; DB 2; Length 646;
Best Local Similarity 75.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXPAE 13
| | | | | | | | |
Db 426 TFCGTTDYLAPE 437

RESULT 4
S55694
protein kinase (EC 2.7.1.37) sck1, cAMP-dependent - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 05-Oct-2004
C:Accession: S55694; T38040
R:Jin, M.; Fujita, M.; Culley, B.M.; Apollinario, E.; Yamamoto, M.; Maundrell, K.; Hoffmann, K.; Hoffmann, K.
Genetics 140, 457-467, 1995
A:Title: sck1, a high copy number suppressor of defects in the cAMP-dependent protein kinase
A:Reference number: S55694; MUID:96120227; PMID:7498728
A:Accession: S55694
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-696 <JIN>
A:Cross-references: UNIPROT:P50530; UNIPARC:UPI00001691AA; GB:D38108; NID:g1136301; PID:g1136301
A:Note: the authors translated the codon GAT for residue 687 as His
R:McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Whitehead, S.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21764
A:Accession: T38040
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-176, 'F', 178-198, 'A', 200-696 <MCD>
A:Cross-references: UNIPARC:UPI000013564D; EMBL:AL109951; PIDN:CAB53053.1; GSPDB:GN00066
A:Experimental source: strain 972h-; cosmid c1B9
C:Genetics:
A:Gene: sck1; SPDB:SPAC1B9.02c
A:Map position: 1
A:Introns: 80/3; 311/1; 633/2
C:Keywords: ATP; phosphotransferase; protein kinase
F:300-563/Domain: protein kinase homology <KIN>
F:308-316/Region: protein kinase ATP-binding motif

Query Match 96.3%; Score 52; DB 2; Length 696;
Best Local Similarity 75.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXPAE 13
| | | | | | | | |
Db 462 TFCGTTDYLAPE 473

RESULT 5
A39616
protein kinase RAD53 (EC 2.7.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein P2586; protein YPL153C; SPK1 protein
C:Species: Saccharomyces cerevisiae
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: A39616; S65164; S69446; S13321
R:Stern, D.F.; Zheng, P.; Beidler, D.R.; Zerillo, C.
Mol. Cell. Biol. 11, 987-1001, 1991
A:Title: Spk1, a new kinase from Saccharomyces cerevisiae, phosphorylates proteins on serine
A:Reference number: A39616; MUID:91117267; PMID:1899289
A:Accession: A39616
A:Molecule type: DNA

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A;Residues: 1-821 <STE>  
A;Cross-references: UNIPROT:P22216; UNIPARC:UPI000005328E; GB:M55623; NID:g172656; PIDN:  
A;Experimental source: strain S288C  
R;Zheng, P.; Fay, D.S.; Burton, J.; Xiao, H.; Pinkham, J.L.; Stern, D.F.  
Mol. Cell. Biol. 13, 5829-5842, 1993  
A;Title: SPK1 is an essential S-phase-specific gene of *Saccharomyces cerevisiae* that encodes  
A;Reference number: A54697; MUID:93361015; PMID:8355715  
A;Contents: annotation  
R;Purnelle, B.; Coster, F.; Goffeau, A.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S65154  
A;Accession: S65164  
A;Molecule type: DNA  
A;Residues: 1-821 <PUR>  
A;Cross-references: UNIPARC:UPI000005328E; EMBL:Z73509; NID:g1370325; PIDN:CAA97858.1; E  
A;Experimental source: strain S288C (AB972)  
R;Purnelle, B.; Coster, F.; Naveau, F.; Goffeau, A.  
submitted to the EMBL Data Library, March 1996  
A;Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies  
a gene to the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant  
A;Reference number: S69428  
A;Accession: S69446  
A;Molecule type: DNA  
A;Residues: 1-821 <PUW>  
A;Cross-references: UNIPARC:UPI000005328E; EMBL:X96770; NID:g1403537; PIDN:CAA65568.1; E  
C;Genetics:  
A;Gene: SGD:RAD53; SPK1; MEC2; SAD1; MIPS:YPL153C  
A;Cross-references: SGD:S0006074; MIPS:YPL153C  
A;Map position: 16L  
C;Function:  
A;Description: serine/threonine-specific protein kinase  
A;Note: contains low activity as tyrosine-specific protein kinase  
C;Superfamily: protein kinase SPK1; kinase interaction domain homology; protein kinase h  
C;Keywords: ATP; cell cycle control; nucleus; phosphotransferase; serine/threonine-speci  
F:68-133/Domain: kinase interaction domain homology <KIH>  
F:196-466/Domain: protein kinase homology <KIN>  
F:204-213/Region: protein kinase ATP-binding motif  
F:227/Active site: Lys #status predicted  
Query Match 96.3%; Score 52; DB 1; Length 821;  
Best Local Similarity 75.0%; Pred. No. 0.047;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXXVAPE 13  
DB 354 TFCGTLAYVAPE 365  
RESULT 6  
S48986  
probable protein kinase SCH9 (EC 2.7.1.1-) - yeast (*Saccharomyces cerevisiae*)  
N;Alternate names: protein YHR205w  
C;Species: *Saccharomyces cerevisiae*  
C;Date: 02-Dec-1994 #sequence\_revision 02-Dec-1994 #text\_change 05-Oct-2004  
C;Accession: S48986; S30022; A28429  
R;Macri, C.  
submitted to the EMBL Data Library, February 1994  
A;Description: The sequence of *S. cerevisiae* cosmid 9177.  
A;Reference number: S46671  
A;Accession: S48986  
A;Molecule type: DNA  
A;Residues: 1-823 <MAC>  
A;Cross-references: UNIPROT:P11792; UNIPARC:UPI0000135644; EMBL:U00029; NID:g551322; PID  
R;di Blas, F.; Carra, E.; de Vendittis, E.; Masturzo, P.; Burderi, E.; Lambrinoudaki, I  
Yeast 9, 21-32, 1993  
A;Title: The SCH9 protein kinase mRNA contains a long 5' leader with a small open reading  
A;Reference number: S30021; MUID:93182531; PMID:8442384  
A;Accession: S30022  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 'M', 1-823 <DIB>  
A;Cross-references: UNIPARC:UPI000016834E; EMBL:X57629; NID:g5277; PIDN:CAA40853.1; PID:  
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1991

R;Toda, T.; Cameron, S.; Sasse, P.; Wigler, M.  
Genes Dev. 2, 517-527, 1988  
A;Title: SCH9, a gene of *Saccharomyces cerevisiae* that encodes a protein distinct from,  
A;Reference number: A28429; MUID:88255839; PMID:3290050  
A;Accession: A28429  
A;Molecule type: DNA  
A;Residues: 'M', 1-364, 'S', 366-749, 'K', 751-823 <TOD>  
A;Cross-references: UNIPARC:UPI0000168B13; EMBL:X12560; NID:g4425; PIDN:CAA31073.1; PID  
C;Genetics:  
A;Gene: SGD:SCH9  
A;Cross-references: SGD:S0001248; MIPS:YHR205w  
A;Map position: 8R  
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
F:409-670/Domain: protein kinase homology <KIN>  
F:417-425/Region: protein kinase ATP-binding motif  
Query Match 96.3%; Score 52; DB 2; Length 823;  
Best Local Similarity 75.0%; Pred. No. 0.047;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXXVAPE 13  
DB 569 TFCGTTEYLAPE 580  
RESULT 7  
T07875  
protein kinase homolog BNPK-3 - rape (fragment)  
C;Species: *Brassica napus* (rape)  
C;Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C;Accession: T07875  
R;Zhou, X.R.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: Z16189  
A;Accession: T07875  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-69 <ZHO>  
A;Cross-references: UNIPROT:Q39300; UNIPARC:UPI000009DC6C; EMBL:U26747; NID:g849146; P  
A;Experimental source: cv. H165; seedlings  
Query Match 94.4%; Score 51; DB 2; Length 69;  
Best Local Similarity 75.0%; Pred. No. 0.0081;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXXVAPE 13  
DB 40 TFCGTPAYVAPE 51  
RESULT 8  
T07876  
protein kinase homolog BNPK-4 - rape (fragment)  
C;Species: *Brassica napus* (rape)  
C;Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
C;Accession: T07876  
R;Zhou, X.R.  
submitted to the EMBL Data Library, May 1995  
A;Reference number: Z16189  
A;Accession: T07876  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-69 <ZHO>  
A;Cross-references: UNIPROT:Q39301; UNIPARC:UPI00000A015B; EMBL:U26748; NID:g849148; P  
A;Experimental source: cv. 165; seedlings  
Query Match 94.4%; Score 51; DB 2; Length 69;  
Best Local Similarity 75.0%; Pred. No. 0.0081;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TFCGTXXXVAPE 13  
DB 40 TFCGTPAYVAPE 51

RESULT 9  
 T07878  
 protein kinase homolog BNPK-5 - rape (fragment)  
 C:Species: Brassica napus (rape)  
 C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 09-Jul-2004  
 C:Accession: T07878  
 R:Zhou, X.R.  
 submitted to the EMBL Data Library, May 1995  
 A:Reference number: Z16189  
 A:Accession: T07878  
 A:Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: mRNA  
 A:Residues: 1-69 <ZHO>  
 A:Cross-references: UNIPROT:Q39302; UNIPARC:UPI00000AB5F3; EMBL:U26749; NID:g849150; PID  
 A:Experimental source: cv. H165; seedlings  
  
 Query Match 94.4%; Score 51; DB 2; Length 69;  
 Best Local Similarity 75.0%; Pred. No. 0.0081; 3; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 TFCGTXXYXAPE 13  
 ||||| ||||  
 Db 40 TFCGTPAYLAPE 51  
  
 RESULT 10  
 S20964  
 ribosomal protein S6 kinase (EC 2.7.1.1-), 70K - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 09-Jul-2004  
 C:Accession: S20964  
 R:Lane, H.A.; Morley, S.J.; Doree, M.; Kozma, S.C.; Thomas, G.  
 EMBO J. 11, 1743-1749, 1992  
 A:Title: Identification and early activation of a Xenopus laevis p70(s6k) following prog  
 A:Reference number: S20964; MUID:92258384; PMID:1374712  
 A:Accession: S20964  
 A:Molecule type: mRNA  
 A:Residues: 1-221 <LAN>  
 A:Cross-references: UNIPROT:Q00603; UNIPARC:UPI00000FDC4D; EMBL:X66179; NID:g64963; PIDN  
 C:Superfamily: ribosomal protein S6 kinase; protein kinase homology  
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
 F:16-221/Domain: protein kinase homology (fragment) <KIN>  
 F:24-32/Region: protein kinase ATP-binding motif  
  
 Query Match 94.4%; Score 51; DB 2; Length 221;  
 Best Local Similarity 75.0%; Pred. No. 0.023;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 TFCGTXXYXAPE 13  
 ||||| ||||  
 Db 179 TFCGTIEYNAPE 190  
  
 RESULT 11  
 S58882  
 protein kinase Cds1 (EC 2.7.1.-) [validated] - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C:Accession: S58882; S71846; T41204; T52473  
 R:Murakami, H.; Okayama, H.  
 Nature 374, 817-819, 1995  
 A:Title: A kinase from fission yeast responsible for blocking mitosis in S phase.  
 A:Reference number: S58882; MUID:95240713; PMID:7723827  
 A:Accession: S58882  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-460 <MUR>  
 A:Cross-references: UNIPROT:Q09170; UNIPARC:UPI00001755F9; EMBL:X85040; NID:g794146  
 R:Murakami, H.  
 submitted to the EMBL Data Library, March 1995  
 A:Reference number: S71846

A:Accession: S71846  
 A:Molecule type: mRNA  
 A:Residues: 1-60,'G',62-202,'I',204-460 <MUR2>  
 A:Cross-references: UNIPARC:UPI00001691A1; EMBL:X85040; NID:g794146; PIDN:CAA59410.1; PI  
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.  
 submitted to the EMBL Data Library, July 1999  
 A:Reference number: Z21978  
 A:Accession: T41204  
 A:Status: translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-202,'I',204-237,'F',239-460 <WOO>  
 A:Cross-references: UNIPARC:UPI0000127455; EMBL:AL109736; NID:g5701956; PIDN:CAB52158.1.  
 A:Experimental source: strain 972h(-); Cosmid c1985  
 R:Indsay, H.D.; Griffiths, D.J.F.; Edwards, R.J.; Christensen, P.U.; Murray, J.M.; Osma  
 Genes Dev. 12, 382-395, 1998  
 A:Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoint  
 A:Reference number: Z26084; MUID:98119835; PMID:9450932  
 A:Accession: T52473  
 A:Status: preliminary; translated from GB/EMBL/DBDJ  
 A:Molecule type: DNA  
 A:Residues: 1-202,'I',204-237,'F',239-460 <LIN>  
 A:Cross-references: UNIPARC:UPI0000127455; EMBL:AJ222869; NID:g2689196; PIDN:CAA11019.1.  
 C:Genetics:  
 A:Gene: SPBC18B5.11c; cds1  
 A:Map position: 3 103/1; 113/3; 142/1; 228/3; 298/3; 368/2  
 A:introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2  
 C:Function:  
 A:Description: EC 2.7.1.-; protein kinase Cds1 [validated, MUID:98119835]; is required t  
 A:Note: Cds1 is phosphorylated and activated by S-phase arrest and activated by DNA dama  
 C:Superfamily: protein kinase Cds1; kinase interaction domain homology; protein kinase h  
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase  
 F:62-133/Domain: kinase interaction domain homology <KIN>  
 F:165-433/Domain: protein kinase homology <KIN>  
 F:173-181/Region: protein kinase ATP-binding motif  
  
 Query Match 94.4%; Score 51; DB 2; Length 460;  
 Best Local Similarity 75.0%; Pred. No. 0.043;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 TFCGTXXYXAPE 13  
 ||||| ||||  
 Db 328 TFCGTMGYLAPE 339  
  
 RESULT 12  
 JE0377  
 p70 S6 kinase (EC 2.7.-.-) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
 C:Accession: JE0377  
 R:Saitoh, M.; ten Dijke, P.; Miyazono, K.; Ichijo, H.  
 Biochem. Biophys. Res. Commun. 253, 470-476, 1998  
 A:Title: Cloning and characterization of p70S6Kbeta defines a novel family of p70 S6 kin  
 A:Reference number: JE0377; MUID:99097259; PMID:9878560  
 A:Accession: JE0377  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-481 <SAI>  
 A:Cross-references: UNIPROT:Q09B0; UNIPARC:UPI0000169453; DBSJ:AB019245; NID:g4165310;  
 C:Superfamily: ribosomal protein S6 kinase; protein kinase homology  
 C:Keywords: phosphotransferase  
  
 Query Match 94.4%; Score 51; DB 2; Length 481;  
 Best Local Similarity 75.0%; Pred. No. 0.045;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 2 TFCGTXXYXAPE 13  
 ||||| ||||  
 Db 227 TFCGTIEYNAPE 238  
  
 RESULT 13  
 T04862

probable serine/threonine-specific protein kinase (EC 2.7.1.1-) F28A21.110 - Arabidopsis  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 05-Oct-2004  
 C;Accession: T04862  
 R;Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999  
 A;Reference number: Z15387  
 A;Accession: T04862  
 A;Molecule type: DNA  
 A;Residues: 1-489 <BEV>  
 A;Cross-references: UNIPROT:Q9SN43; UNIPARC:UPI00000AC648; EMBL:AL035526  
 A;Experimental source: cultivar Columbia; BAC clone F28A21  
 C;Genetics:  
 A;Map position: 4  
 A;Note: F28A21.110  
 C;Keywords: phosphotransferase; protein kinase

Query Match 94.4%; Score 51; DB 2; Length 489;  
 Best Local Similarity 75.0%; Pred. No. 0.046;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXYPE 13  
 ||||| |||||  
 Db 184 TFCGTPAYVAPE 195

RESULT 14  
 T02306  
 N;Alternate names: [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 05-Oct-2004  
 C;Accession: T02306; D84753  
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul, submitted to the EMBL Data Library, July 1998  
 A;Description: Arabidopsis thaliana chromosome II BAC F13P17 genomic sequence.  
 A;Reference number: Z14657  
 A;Accession: T02306  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-502 <ROU>  
 A;Cross-references: UNIPROT:Q22971; UNIPARC:UPI00000A39B8; EMBL:AC004481; NID:g3337347;  
 A;Experimental source: cultivar Columbia  
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A;Reference number: A84420; MUID:20083487; PMID:10617197  
 A;Accession: D84753  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-502 <STO>  
 A;Cross-references: UNIPARC:UPI00000A39B8; GB:AE002093; NID:g3337349; PIDN:AAC27394.1; G  
 C;Genetics:  
 A;Map position: 2  
 F;55-311/domain: protein kinase homology <KIN>

Query Match 94.4%; Score 51; DB 2; Length 502;  
 Best Local Similarity 75.0%; Pred. No. 0.047;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXYPE 13  
 ||||| |||||  
 Db 215 TFCGTPAYVAPE 226

RESULT 15  
 G86414  
 N;Alternate names: [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 05-Oct-2004

C;Accession: G86414  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: G86414  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-520 <STO>  
 A;Cross-references: UNIPROT:Q9LP51; UNIPARC:UPI00000AA794; GB:AE005172; NID:g9502417; P  
 C;Genetics:  
 A;Map position: 1

Query Match 94.4%; Score 51; DB 2; Length 520;  
 Best Local Similarity 75.0%; Pred. No. 0.048;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXYPE 13  
 ||||| |||||  
 Db 232 TFCGTPAYVAPE 243

RESULT 16  
 A41687  
 N;Alternate names: insulin/mitogen-activated cytosolic p70 S6 kinase (S6K); nuclear p85  
 C;Contains: ribosomal protein S6 kinase short splice form; ribosomal protein S6 kinase, C;Species: Homo sapiens (man)  
 C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
 C;Accession: A41687; B41687  
 R;Grove, J.R.; Banerjee, P.; Balasubramanyam, A.; Coffey, P.J.; Price, D.J.; Avruch, J. J. Mol. Cell. Biol. 11, 5541-5550, 1991  
 A;Title: Cloning and expression of two human p70 S6 kinase polypeptides differing only  
 A;Reference number: A41687; MUID:92017834; PMID:1922062  
 A;Accession: A41687  
 A;Molecule type: mRNA  
 A;Residues: 1-525 <GRO1>  
 A;Cross-references: UNIPROT:P23443; UNIPARC:UPI000013C873; GB:M60724; NID:g189507; PIDN  
 A;Accession: B41687  
 A;Molecule type: mRNA  
 A;Residues: 24-525 <GRO2>  
 A;Cross-references: UNIPARC:UPI000012DB33; GB:M60725; NID:g189509; PIDN:AAA36411.1; PID  
 C;Comment: This enzyme phosphorylates ribosomal protein S6 (see PIR:R3HU6). The long sp  
 C;Genetics:  
 A;Gene: GDB:RPS6KB1  
 A;Cross-references: GDB:365650  
 C;Complex: monomer  
 C;Function:  
 A;Description: catalyzes the phosphorylation by ATP of specific serine residues in ribo  
 A;Note: reversibly activated by phosphorylation  
 C;Superfamily: ribosomal protein S6 kinase; protein kinase homology  
 C;Keywords: alternative initiators; ATP; monomer; nucleus; phosphoprotein; phosphotrans  
 F;1-525/Product: ribosomal protein S6 kinase, long splice form #status predicted <SFL>  
 F;2-19/Region: nuclear location signal  
 F;24-525/Product: ribosomal protein S6 kinase, short splice form #status predicted <SFS>  
 F;89-352/Domain: protein kinase homology <KIN>  
 F;97-105/Region: protein kinase ATP-binding motif  
 F;423-450/Region: autoinhibitory  
 F;434,441,447,452/Binding site: phosphate (Thr) (covalent) #status predicted  
 F;444/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 94.4%; Score 51; DB 1; Length 525;  
 Best Local Similarity 75.0%; Pred. No. 0.049;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXXYPE 13

Db 252 TFCGTIEYNAPE 263  
||||| | |||  
Best Local Similarity 75.0%; Pred. No. 0.049;  
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

RESULT 17  
S12906  
probable ribosomal protein S6 kinase (EC 2.7.1.-), 59K - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S12906  
R:Harman, B.; Killmann, M.W.  
FEBS Lett. 273, 248-252, 1990  
A:Title: cDNA encoding a 59 kDa homolog of ribosomal protein S6 kinase from rabbit liver  
A:Reference number: S12906; MUID:91032193; PMID:1699810  
A:Accession: S12906  
A:Molecule type: mRNA  
A:Residues: 1-525 <HAR>  
A:Cross-references: UNIPROT:P21425; UNIPARC:UPI000014C947; EMBL:X54415; NID:g1561; PIDN:  
C:Superfamily: ribosomal protein S6 kinase; protein kinase homology  
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F:89-352/Domain: protein kinase homology <KIN>  
F:97-105/Region: protein kinase ATP-binding motif

Query Match 94.4%; Score 51; DB 1; Length 525;  
Best Local Similarity 75.0%; Pred. No. 0.049;  
Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| | |||  
Db 252 TFCGTIEYNAPE 263

RESULT 18  
TVRTK6  
ribosomal protein S6 kinase (EC 2.7.1.-), 70K - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: A36484; A34992; A38279  
R:Banerjee, P.; Ahmad, M.F.; Grove, J.R.; Kozlosky, C.; Price, D.J.; Avruch, J.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8550-8554, 1990  
A:Title: Molecular structure of a major insulin/mitogen-activated 70-kDa S6 protein kinase  
A:Reference number: A36484; MUID:91046033; PMID:2236064  
A:Accession: A36484  
A:Molecule type: mRNA  
A:Residues: 1-525 <BAN>  
A:Cross-references: UNIPROT:P21425; UNIPARC:UPI0000167985; GB:M58340; GB:M37777; NID:g20  
A:Accession: A34992  
A:Molecule type: protein  
A:Residues: 57-64;105-108,195,'S',197-202;206-223;262-264;336-353;438-442;444-450;492,'X  
A:Cross-references: UNIPARC:UPI0000172SA0; UNIPARC:UPI0000172SA1; UNIPARC:UPI0000172SA2;  
SAY; UNIPARC:UPI0000172SA8; UNIPARC:UPI0000172SA9  
R:Kozma, S.C.; Ferrari, S.; Bassand, P.; Slegmann, M.; Totty, N.; Thomas, G.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7365-7369, 1990  
A:Title: Cloning of the mitogen-activated S6 kinase from rat liver reveals an enzyme of  
A:Reference number: A38279; MUID:91017506; PMID:1699226  
A:Accession: A38279  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 24-366,'P',368-525 <KOZ>  
A:Cross-references: UNIPARC:UPI000012DB34; GB:M57428; GB:M35864; NID:g206839; PIDN:AAA42  
C:Superfamily: ribosomal protein S6 kinase; protein kinase homology  
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F:1-88/Domain: amino-terminal <NTD>  
F:29-46/Region: acidic  
F:89-352/Domain: protein kinase homology <KIN>  
F:97-105/Region: protein kinase ATP-binding motif  
F:353-420/Domain: catalytic domain extension <CDE>  
F:421-525/Domain: carboxyl-terminal <CTD>  
F:123/Active site: Lys #status predicted  
F:434,441,447,452/Binding site: phosphate (Ser) (covalent) #status predicted  
F:444/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 94.4%; Score 51; DB 1; Length 525;

Best Local Similarity 75.0%; Pred. No. 0.049;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| | |||  
Db 252 TFCGTIEYNAPE 263

RESULT 19  
T31529  
hypothetical protein Y47D3A.16 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31529  
R:Matthews, L.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21043  
A:Accession: T31529  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-580 <WIL>  
A:Cross-references: UNIPROT:Q9NAH6; UNIPARC:UPI000007A583; EMBL:AL117202; PIDN:CAB55075  
A:Experimental source: clone Y47D3A  
C:Genetics:  
A:Gene: CESP:Y47D3A.16  
A:Introns: 22/2; 43/3; 96/3; 442/2; 550/2  
C:Superfamily: ribosomal protein S6 kinase; protein kinase homology

Query Match 94.4%; Score 51; DB 2; Length 580;  
Best Local Similarity 75.0%; Pred. No. 0.053;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| | |||  
Db 244 TFCGTIEYNAPE 255

RESULT 20  
KIMSCD  
protein kinase C (EC 2.7.1.-) delta - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 05-Oct-2004  
C:Accession: A40281; S19709  
R:Mischak, H.; Bodenteich, A.; Kolch, W.; Goodnight, J.; Hofer, F.; Mushinski, J.F.  
Biochemistry 30, 7925-7931, 1991  
A:Title: Mouse protein kinase C-delta, the major isoform expressed in mouse hemopoietic  
A:Reference number: A40281; MUID:91329364; PMID:1868068  
A:Accession: A40281  
A:Molecule type: mRNA  
A:Residues: 1-674 <MIS>  
A:Cross-references: UNIPROT:P28867; UNIPARC:UPI000016CFBD; GB:M69042; NID:g200380; PIDN:  
R:Mizuno, K.; Kubo, K.; Saido, T.C.; Akita, Y.; Osada, S.; Kuroki, T.; Ohno, S.; Suzuki,  
Eur. J. Biochem. 202, 931-940, 1991  
A:Title: Structure and properties of a ubiquitously expressed protein kinase C, nPKCdelta  
A:Reference number: S19709; MUID:92111544; PMID:1765103  
A:Accession: S19709  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-318,'E',320-329,'G',331-336,'E',338-500,'G',502,'A',504-512,'I',514-674 <M  
A:Cross-references: UNIPARC:UPI0000028PFD; EMBL:X60304; NID:G53436; PIDN:CAA42845.1; PID  
C:Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-  
of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester  
C:Superfamily: protein kinase C, delta/epsilon/eta/cheta types; protein kinase C zinc-bi  
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf  
F:144-149/Region: pseudophosphorylation motif  
F:159-208/Domain: protein kinase C zinc-binding repeat homology <KZ1>  
F:231-280/Domain: protein kinase C zinc-binding repeat homology <KZ2>  
F:353-601/Region: protein kinase ATP-binding motif  
F:159,189,192,208/Binding site: zinc (His, Cys, Cys, Cys)  
F:172,175,197,200/Binding site: zinc (Cys, Cys, His, Cys, Cys)  
F:231,261,264,280/Binding site: zinc (His, Cys, Cys, Cys)  
F:244,247,269,272/Binding site: zinc (Cys, Cys, His, Cys)

F:376/Active site: Lys #status predicted

Query Match 94.4%; Score 51; DB 1; Length 574;  
Best Local Similarity 75.0%; Pred. No. 0.061;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 505 TFCGTPDYSAPE 516

## RESULT 21

A53530  
protein kinase C (EC 2.7.1.-) epsilon-related - Caenorhabditis elegans  
N;Alternate names: protein kinase C PKCIB, neuronal  
C;Species: Caenorhabditis elegans  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Oct-2004  
C;Accession: A53530  
R;Land, M.; Islas-Trejo, A.; Freedman, J.H.; Rubin, C.S.  
J. Biol. Chem. 269, 9234-9244, 1994  
A;Title: Structure and expression of a novel, neuronal protein kinase C (PKCIB) from Caenorhabditis elegans.  
A;Reference number: A53530; MUID:94179345; PMID:8132661  
A;Accession: A53530  
A;Molecule type: mRNA  
A;Residues: 1-707 <LAN>  
A;Cross-references: UNIPROT:P34895; UNIPARC:UPI000012DFSP; GB:U00181; NID:G484065; PIDN:G484065  
C;Genetics:  
A;Gene: kin-13  
A;Map position: V  
A;Note: located near myo-3, col-1, and CPROT/2 genes

C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate  
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacylglycerol  
C;Superfamily: protein kinase C, delta/epsilon/eta/theta types; protein kinase C zeta/beta types  
C;Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransferase  
F:157-162/Region: pseudophosphorylation motif  
F:171-220/Domain: protein kinase C zinc-binding repeat homology <K21>  
F:249-298/Domain: protein kinase C zinc-binding repeat homology <K22>  
F:376-638/Domain: protein kinase C zinc-binding repeat homology <KIN>  
F:384-392/Region: protein kinase ATP-binding motif  
F:171,201,204,220/Binding site: zinc (His, Cys, Cys)  
F:184,187,209,212/Binding site: zinc (Cys, Cys, His, Cys)  
F:249,279,282,298/Binding site: zinc (His, Cys, Cys, Cys)  
F:262,265,287,290/Binding site: zinc (Cys, Cys, His, Cys)  
F:407,426,502,504/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 94.4%; Score 51; DB 1; Length 707;  
Best Local Similarity 75.0%; Pred. No. 0.064;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 536 TFCGTPDYTAPE 547

## RESULT 22

T16679  
hypothetical protein R04A9.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T16679  
R;Geisels, C.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid R04A9.  
A;Reference number: Z18558  
A;Accession: T16679  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-780 <GE1>  
A;Cross-references: UNIPROT:Q21694; UNIPARC:UPI000017CD4D; EMBL:U41550; NID:g1118045; PIDN:G1118045  
C;Genetics:  
A;Gene: CESP:R04A9.5

A;Introns: 36/3; 326/3; 349/3; 377/3; 396/3; 428/3; 484/1; 515/1; 632/3; 671/1; 752/3

Query Match 94.4%; Score 51; DB 2; Length 780;  
Best Local Similarity 75.0%; Pred. No. 0.069;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 184 TFCGTHEYMAPE 195

## RESULT 23

A60543  
protein kinase (EC 2.7.1.37), CAMP-dependent, catalytic chain - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: A60543  
R;Roth, J.S.; Heieh, L.L.; Peraino, C.; Weinstein, I.B.  
Cancer Res. 50, 1675-1680, 1990  
A;Title: Isolation of a complementary DNA encoding the catalytic subunit of protein kinase C.  
A;Reference number: A60543; MUID:90167652; PMID:2306720  
A;Accession: A60543  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-334 <ROT>  
A;Cross-references: UNIPROT:Q05759; UNIPARC:UPI000008E0C6; GB:X53261; NID:G288119; PIDN:G288119  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; CAMP binding; phosphotransferase; serine/threonine-specific protein kinase  
F:25-281/Domain: protein kinase homology <KIN>  
F:33-41/Region: protein kinase ATP-binding motif

Query Match 92.6%; Score 50; DB 2; Length 334;  
Best Local Similarity 75.0%; Pred. No. 0.051;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 181 TFCGTPYLAPE 192

## RESULT 24

T26334  
hypothetical protein W10G6.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 05-Oct-2004  
C;Accession: T26334  
R;McMurray, A.  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z20201  
A;Accession: T26334  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-422 <WIL>  
A;Cross-references: UNIPROT:Q94365; UNIPARC:UPI000007852E; EMBL:Z81140; PIDN:CAB03485.1  
A;Experimental source: clone W10G6  
C;Genetics:  
A;Gene: CESP:W10G6.2  
A;Map position: X  
A;Introns: 14/3; 60/2; 88/2; 135/3; 179/3; 217/2; 290/3; 393/1

Query Match 92.6%; Score 50; DB 2; Length 422;  
Best Local Similarity 75.0%; Pred. No. 0.062;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 252 TFCGTPYLAPE 263

## RESULT 25

T11854  
protein kinase (EC 2.7.1.-) - Trypanosoma brucei  
C;Species: Trypanosoma brucei

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 05-Oct-2004  
C:Accession: T11854  
R:Gale, M.J.; Parsons, M.  
Mol. Biochem. Parasitol. 59, 111-122, 1993  
A:Title: Trypanosoma brucei gene family encoding protein kinases with catalytic domains  
A:Reference number: Z17363; MUID:93295429; PMID:8515773  
A:Accession: T11854  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-431 <GAL>  
A:Cross-references: UNIPROT:Q08942; UNIPARC:UPI0000130511; EMBL:L03778; NID:g162169; PID  
C:Genetics:  
A:Note: nrka  
C:Keywords: ATP; phosphotransferase

Query Match 92.6%; Score 50; DB 2; Length 431;  
Best Local Similarity 75.0%; Pred. No. 0.063;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| |  
Db 183 TFCGTPXYLAPE 194

RESULT 26  
A48094  
serum and glucocorticoid-regulated kinase - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 31-Dec-2004  
C:Accession: A48094  
R:Webster, M.K.; Goya, L.; Ge, Y.; Maiyar, A.C.; Firestone, G.L.  
Mol. Cell. Biol. 13, 2031-2040, 1993  
A:Title: Characterization of sgk, a novel member of the serine/threonine protein kinase  
A:Reference number: A48094; MUID:93204949; PMID:8455596  
A:Accession: A48094  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-431 <WEB>  
A:Cross-references: UNIPARC:UPI000017A3E8  
A:Experimental source: Con8.hd6 mammary epithelial tumor cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:127618, NCBI:P:127619)  
C:Keywords: ATP  
F:96-355/Domain: protein kinase homology <KIN>  
F:104-112/Region: protein kinase ATP-binding motif

Query Match 92.6%; Score 50; DB 2; Length 431;  
Best Local Similarity 75.0%; Pred. No. 0.063;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| |  
Db 256 TFCGTPEYLAPE 267

RESULT 27  
JC4345  
protein kinase (EC 2.7.1.37) akt3 [validated] - rat  
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C:Accession: JC4345  
R:Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; K  
Biochem. Biophys. Res. Commun. 216, 526-534, 1995  
A:Title: Molecular cloning and characterization of a new member of the RAC protein kinase  
e C subpecies and beta gamma subunits of G proteins.  
A:Reference number: JC4345; MUID:96063640; PMID:7488143  
A:Accession: JC4345  
A:Molecule type: mRNA  
A:Residues: 1-454 <KON>  
A:Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DDBJ:D49836; NID:g1136777; PI  
A:Experimental source: brain  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protei  
F:4-105/Domain: pleckstrin repeat homology <PLK>  
F:146-405/Domain: protein kinase homology <KIN>  
F:154-162/Region: protein kinase ATP-binding motif  
F:177/Active site: Lys #status predicted

Query Match 92.6%; Score 50; DB 1; Length 454;  
Best Local Similarity 75.0%; Pred. No. 0.066;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| |  
Db 305 TFCGTPEYLAPE 316

RESULT 28  
T17287  
protein kinase (EC 2.7.1.37) akt3 short splice form - human  
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C:Accession: T17287  
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, September 1999  
A:Reference number: Z18723  
A:Accession: T17287  
A:Molecule type: mRNA  
A:Residues: 1-462 <POU>  
A:Cross-references: UNIPARC:UPI000016AC77; EMBL:AL117525; GB:CAB55977; NID:g5912043; PID  
A:Experimental source: adult testis; clone DKFZp34N0250  
R:Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.  
J. Biol. Chem. 274, 21528-21532, 1999  
A:Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and andrpg  
A:Reference number: A64199; PMID:10419456  
A:Contents: annotation  
C:Comment: This protein is increased in estrogen receptor-negative breast cancers and an  
C:Genetics:  
A:Gene: GDB:AKT3  
A:Cross-references: GDB:9954867  
A:Map position: 1q44-1q44  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protei  
F:4-105/Domain: pleckstrin repeat homology <PLK>  
F:146-405/Domain: protein kinase homology <KIN>  
F:154-162/Region: protein kinase ATP-binding motif  
F:177/Active site: Lys #status predicted

Query Match 92.6%; Score 50; DB 1; Length 462;  
Best Local Similarity 75.0%; Pred. No. 0.067;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
||||| |  
Db 305 TFCGTPEYLAPE 316

RESULT 29  
A59380  
protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human  
N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific prote  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
A:Accession: A59380; A59379  
R:Brodebeck, D.; Cron, P.; Hemmings, B.A.  
J. Biol. Chem. 274, 9133-9136, 1999  
A:Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti  
A:Reference number: A59380; MUID:99194749; PMID:10092583  
A:Accession: A59380

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-479 <BRO>  
A:Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI0000033588; GB:AAD29089; NID:g4757579; P1  
P:Masure, S.; Haefner, B.; Wesseling, J.J.; Hoefnagel, E.; Mortier, E.; Verhaselt, P.;  
Eur. J. Biochem. 265, 353-360, 1999  
A>Title: Molecular cloning, expression and characterization of the human serine/threonine  
A:Reference number: A59379; MUID:99421751; PMID:10491192  
A:Accession: A59379  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-479 <MAS>  
A:Cross-references: UNIPARC:UPI0000033588; GB:CAB53537; NID:g5804886; PIDN:CAB53537.1  
C:Genetics:  
A:Gene: GDB:AKT3; PKBG: PKBG; RAC-gamma  
A:Cross-references: GDB:9954867  
A:Map position: 1q44-1q44  
C:Function:  
A>Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F:7-108/Domain: pleckstrin repeat homology <PLK>  
F:149-408/Domain: protein kinase ATP-binding motif  
F:157-165/Region: protein kinase ATP-binding motif  
F:177/Active site: Lys #status predicted  
F:305/Binding site: phosphate (Thr) (covalent) #status predicted  
F:474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 92.6%; Score 50; DB 1; Length 479;  
Best Local Similarity 75.0%; Pred. No. 0.07;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 305 TFCGTPEYLAPE 316

RESULT 30  
A38578  
protein kinase 2 (EC 2.7.1.-) - slime mold (Dictyostelium discoideum)  
C:Species: Dictyostelium discoideum  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 31-Dec-2004  
C:Accession: A38578  
R:Haribabu, B.; Dottin, R.P.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1115-1119, 1991  
A>Title: Identification of a protein kinase multigene family of Dictyostelium discoideum  
A:Reference number: A38578; MUID:91142122; PMID:1996312  
A:Accession: A38578  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-479 <R>  
A:Cross-references: UNIPROT:P28178; UNIPARC:UPI0000131858; GB:M59744; NID:g167717; PIDN:  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; serine/threonine  
F:151-407/Domain: protein kinase homology <KIN>  
F:159-167/Region: protein kinase ATP-binding motif

Query Match 92.6%; Score 50; DB 2; Length 479;  
Best Local Similarity 75.0%; Pred. No. 0.07;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 309 TFCGTPEYLAPE 320

RESULT 31  
A39360  
protein kinase (EC 2.7.1.37) akt1 [validated] - human  
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C:Species: Homo sapiens (man)  
C:Date: 20-Mar-1992 #sequence\_revision 12-May-1994 #text\_change 16-Aug-2004  
C:Accession: A39360; S36389; S18000; S20836

R:Jones, P.F.; Jakubowicz, T.; Pitossi, F.J.; Maurer, F.; Hemmings, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991  
A>Title: Molecular cloning and identification of a serine/threonine protein kinase of t  
A:Reference number: A39360; MUID:91239529; PMID:1851997  
A:Accession: A39360  
A:Molecule type: mRNA  
A:Residues: 1-480 <JON>  
A:Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E75B; GB:M63167; NID:g190827; PIDN:  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A:Reference number: S24423; MUID:92249329; PMID:1533586  
A:Contents: erratum  
A:Accession: S36389  
A:Molecule type: mRNA  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '  
A:Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:g35480; PIDN:CAA43372.1; P1  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991  
A>Note: this is a revision to the sequence from reference S17999  
R:Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A>Title: Molecular cloning and characterisation of a novel putative protein-serine kina  
A:Reference number: S17999; MUID:92037600; PMID:1718748  
A:Accession: S18000  
A:Molecule type: mRNA  
A:Residues: 63-70, 'TPSSAACSGPLSSNAPSMWRLRSGGVNHRHPCGRRPQ', 'EAGGGDGLPVGLTORLGRRRDGG'  
A:Cross-references: UNIPARC:UPI00001725AB; EMBL:X61037  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991  
A>Note: this sequence has been revised in reference S24423  
R:Coffer, P.  
submitted to the EMBL Data Library, July 1991  
A:Reference number: S20836  
A:Accession: S20836  
A:Molecule type: mRNA  
A:Residues: 63-70, 'TPSSAACSGPLSSNAPSMWRLRSGGVNHRHPCGRRPQ', 'EAGGGDGLPVGLTORLGRRRDGG'  
A:Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037  
A>Note: this sequence has been revised in reference S24423  
R:Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemmin  
EMBO J. 15, 6541-6551, 1996  
A>Title: Mechanism of activation of protein kinase B by insulin and IGF-1.  
A:Reference number: A64192; MUID:97133284; PMID:8978681  
A:Contents: annotation; autophosphorylation site  
C:Contents: annotation; phosphorylation sites  
R:Tokar, A.; Newton, A.C.  
J. Biol. Chem. 275, 8271-8274, 2000  
A>Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical P  
A:Reference number: A64193; MUID:20187529; PMID:10722653  
A:Contents: annotation; autophosphorylation site  
C:Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidyl-  
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.  
C:Genetics:  
A:Gene: GDB:AKT1; RAC; PKB  
A:Cross-references: GDB:118989; OMIM:164730  
A:Map position: 14q32.32-14q32.32  
C:Function:  
A>Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A:Pathway: signal transduction pathways regulating various processes including insulin  
e production  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen  
F:4-106/Domain: pleckstrin repeat homology <PLK>  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:179/Active site: Lys #status predicted  
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein k  
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experim.

Query Match 92.6%; Score 50; DB 1; Length 480;  
Best Local Similarity 75.0%; Pred. No. 0.07;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXXYXAPE 13  
|||||  
Db 309 TFCGTPEYLAPE 320

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Db          308 TFCGTPEYLAPE 319
;
RESULT 32
JC2437
protein kinase (EC 2.7.1.37) akt1 [validated] - rat
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: JC2437
R:Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.
Biochem. Biophys. Res. Commun. 205, 817-825, 1994
A:Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associati
A:Reference number: JC2437; MUID:95091823; PMID:7999118
A:Accession: JC2437
A:Molecule type: mRNA
A:Residues: 1-480 <KON>
A:Cross-references: UNIPROT:P47196; UNIPARC:UPI000012E044; DDBJ:D30040; NID:g485402; PID
A:Experimental source: testis
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match          92.6%; Score 50; DB 1; Length 480;
Best Local Similarity 75.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          2 TFCGTXXYXAPE 13
||||| |||
Db          308 TFCGTPEYLAPE 319

RESULT 33
S33364
protein kinase (EC 2.7.1.37) akt1 [similarity] - mouse
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: S33364
R:Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner, J
Oncogene 8, 745-754, 1993
A:Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt a
A:Reference number: S33364; MUID:93173519; PMID:8437858
A:Accession: S33364
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-480 <BEL>
A:Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID
C:Genetics:
A:Gene: MGI:Akt
A:Cross-references: MGI:87986
A:Map position: 12
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match          92.6%; Score 50; DB 1; Length 480;

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Best Local Similarity 75.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          2 TFCGTXXYXAPE 13
||||| |||
Db          308 TFCGTPEYLAPE 319

RESULT 34
S62117
protein kinase (EC 2.7.1.37) akt1 [similarity] - bovine
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C:Accession: S62117; S24423; S17999; S15714; S36388
R:Coffer, P.J.; Woodgett, J.R.
submitted to the EMBL Data Library, December 1991
A:Reference number: S62117
A:Accession: S62117
A:Molecule type: mRNA
A:Residues: 1-480 <COF>
A:Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012E042; EMBL:X61036; NID:g630; PID:N
A:Note: this is a revision to the sequence from reference S17999
R:Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A:Reference number: S24423; MUID:92249329; PMID:1533586
A:Accession: S24423
A:Contents: erratum
A:Molecule type: mRNA
A>Status: nucleic acid sequence not shown
A:Residues: 70-78, 'N', 80-145 <CON>
A:Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036
A:Note: this is a revision to the sequence from reference S17999
R:Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A:Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
A:Reference number: S17999; MUID:920337600; PMID:1718748
A:Accession: S17999
A:Molecule type: mRNA
A:Residues: 1-70, 'TPSSSAACGPRSSARSSTWRRSPGGVDRHPDGRRAQAGGGDGLPVGLTRRELGGRGDVAGQA
A:Cross-references: UNIPARC:UPI00001725AE; EMBL:X61036
A:Note: this sequence has been revised in references S62117 and S24423
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating various processes
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F:4-106/Domain: pleckstrin repeat homology <PLK>
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:179/Active site: Lys #status predicted
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match          92.6%; Score 50; DB 1; Length 480;
Best Local Similarity 75.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY          2 TFCGTXXYXAPE 13
||||| |||
Db          308 TFCGTPEYLAPE 319

RESULT 35
A46288
protein kinase (EC 2.7.1.37) akt2 - human
N:Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein
C:Species: Homo sapiens (man)
C>Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C:Accession: A46288
R:Cheng, J.O.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.;
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
A:Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/th

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A:Reference number: A46288; MUID:93028445; PMID:1409633

A:Accession: A46288

A:Molecule type: mRNA

A:Residues: 1-481 <CHE>

A:Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:gl178325; PIDN:  
A>Note: sequence extracted from NCBI backbone (NCBIP:115859)

C:Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.

C:Genetics:

A:Gene: GDB:AKT2

A:Cross-references: GDB:l135660; OMIM:164731

A:Map position: 19q13.2-19q13.2

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating various processes

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F;4-106/Domain: pleckstrin repeat homology <PLK>

F;150-409/Domain: protein kinase homology <KIN>

F;158-166/Region: protein kinase ATP-binding motif

F;181/Active site: Lys #status predicted

Query Match 92.6%; Score 50; DB 1; Length 481;

Best Local Similarity 75.0%; Pred. No. 0.07;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13

||||| |||

DB 309 TFCGTPEYLAPE 320

RESULT 36

JC2438

protein kinase [EC 2.7.1.37] akt2 [validated] - rat

N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004

C:Accession: JC2438

R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.

Biochem. Biophys. Res. Commun. 205, 817-825, 1994

A:Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associatio

A:Reference number: JC2437; MUID:95091823; PMID:7999118

A:Accession: JC2438

A:Molecule type: mRNA

A:Residues: 1-481 <KON>

A:Cross-references: UNIPROT:P47197; UNIPARC:UPI000012577B; DDBJ:D30041; NID:g485404; PID

A:Experimental source: testis

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating various processes including myoblast

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F;4-106/Domain: pleckstrin repeat homology <PLK>

F;150-409/Domain: protein kinase homology <KIN>

F;158-166/Region: protein kinase ATP-binding motif

F;181/Active site: Lys #status predicted

Query Match 92.6%; Score 50; DB 1; Length 481;

Best Local Similarity 75.0%; Pred. No. 0.07;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13

||||| |||

DB 309 TFCGTPEYLAPE 320

RESULT 37

T43234

protein kinase [EC 2.7.1.37] akt-2 short splice form [similarity] - Caenorhabditis eleg

N;Alternate names: PKB; protein kinase B

C:Species: Caenorhabditis elegans

C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004

C:Accession: T43234

R;Paradis, S.; Ruvkun, G.

Genes Dev. 12, 2488-2498, 1998

A:Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from Akt

A:Reference number: Z22355; MUID:98382502; PMID:9716402

A:Accession: T43234

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-483 <PAR>

A:Cross-references: UNIPROT:O77145; UNIPARC:UPI000007ABA0; EMBL:AF072381; NID:g3694832;

C:Genetics:

A:Gene: akt-2

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating metabolism, development, and longevi

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C:Keywords: alternative splicing; ATP; phosphoprotein; phosphotransferase; serine/threoo

F;11-113/Domain: pleckstrin repeat homology <PK>

F;178-437/Domain: protein kinase homology <KIN>

F;186-194/Region: protein kinase ATP-binding motif

F;209/Active site: Lys #status predicted

F;337/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 92.6%; Score 50; DB 1; Length 483;

Best Local Similarity 75.0%; Pred. No. 0.07;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TFCGTXYYXAPE 13

||||| |||

DB 337 TFCGTPEYLAPE 348

RESULT 38

T21523

protein kinase [EC 2.7.1.37] akt-2 long splice form [similarity] - Caenorhabditis eleg

N;Alternate names: PKB; protein kinase B

C:Species: Caenorhabditis elegans

C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004

C:Accession: T21523; T23878

R;McMurray, A.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z19434

A:Accession: T21523

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-528 <WIL>

A:Cross-references: UNIPROT:Q9XTG7; UNIPARC:UPI0000076045; EMBL:AL031621; PIDN:CAA20936

A:Experimental source: clone F28H6

R;McMurray, A.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z19812

A:Accession: T23878

A>Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-528 <W12>

A:Cross-references: UNIPARC:UPI0000076045; EMBL:Z92837; PIDN:CAB07403.1; GSPDB:GN000028;

A:Experimental source: clone R03E1

C:Genetics:

A:Gene: akt-2; CESP:F28H6.1

A:Map position: X

A:Introns: 32/2; 68/3; 135/3; 175/3; 241/3; 285/2; 305/3; 348/3; 469/3

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

A:Pathway: signal transduction pathways regulating metabolism, development, and longevi

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein

C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotran

F;11-113/Domain: pleckstrin repeat homology <KIN>

F;178-437/Domain: protein kinase homology <KIN>

F;186-194/Region: protein kinase ATP-binding motif

F;209/Active site: Lys #status predicted

F;337/Binding site: phosphate (Thr) (covalent) #status predicted

F;505/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predict

Query Match 92.6%; Score 50; DB 1; Length 528;

Best Local Similarity 75.0%; Pred. No. 0.076;

```

Matches      9;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

QY      2  TFCGTXXXYAPE 13
      |||||  ||||
Db      337  TFCGTPPEYLAPE 348

RESULT 39
T43232
protein kinase (EC 2.7.1.37) akt-1 splice form a [similarity] - Caenorhabditis elegans
N:Alternate names: PKB; protein kinase B
C:Species: Caenorhabditis elegans
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: T43232; T19224
R:Paradis, S.; Ruvkun, G.
Genes Dev. 12, 2488-2498, 1998
A:Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AQ
A:Reference number: 222355; MUID:98382502; PMID:9716402
A:Accession: T43232
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-541 <PAR>
A:Cross-references: UNIPROT:Q17941; UNIPARC:UPI0000080469; EMBL:AF072379; NID:G3694828;
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19092
A:Accession: T19224
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Cross-references: UNIPARC:UPI0000080469; EMBL:CAA98240.1; GSPDB:GN000023;
A:Experimental source: clone C12D8
C:Genetics:
A:Gene: akt-1; C12D8.10
A:Map position: 5
A:Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 318/3; 361/3; 482/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating metabolism, development, and longevit
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
F:14-116/Domain: pleckstrin repeat homology <PLK>
F:191-450/Domain: protein kinase homology <KIN>
F:199-207/Region: protein kinase ATP-binding motif
F:222/Active site: Lys #status predicted
F:350/Binding site: phosphate (Thr) (covalent) #status predicted
F:517/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match      92.6%; Score 50; DB 1; Length 541;
Best Local Similarity 75.0%; Pred. No. 0.078;
Matches      9;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

QY      2  TFCGTXXXYAPE 13
      |||||  ||||
Db      350  TFCGTPPEYLAPE 361

RESULT 40
T43233
protein kinase (EC 2.7.1.37) akt-1 splice form b [similarity] - Caenorhabditis elegans
N:Alternate names: PKB; protein kinase B
C:Species: Caenorhabditis elegans
C:Date: 31-Mar-2001 #sequence_revision 31-Mar-2001 #text_change 16-Aug-2004
C:Accession: T43233; T19222
R:Paradis, S.; Ruvkun, G.
Genes Dev. 12, 2488-2498, 1998
A:Title: Caenorhabditis elegans Akt/PKB transduces insulin receptor-like signals from AQ
A:Reference number: 222355; MUID:98382502; PMID:9716402
A:Accession: T43233
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-546 <PAR>
A:Cross-references: UNIPROT:Q17942; UNIPARC:UPI00000756DF; EMBL:AF072380; NID:G3694830;

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R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19092
A:Accession: T19222
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-546 <WIL>
A:Cross-references: UNIPARC:UPI00000756DF; EMBL:CAA98238.1; GSPDB:GN000023;
A:Experimental source: clone C12D8
C:Genetics:
A:Gene: akt-1; C12D8.10
A:Map position: 5
A:Introns: 35/2; 71/3; 134/3; 188/3; 254/3; 323/3; 366/3; 487/3
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A:Pathway: signal transduction pathways regulating metabolism, development, and longevit
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotrans
F:14-116/Domain: pleckstrin repeat homology <PLK>
F:191-455/Domain: protein kinase homology <KIN>
F:199-207/Region: protein kinase ATP-binding motif
F:222/Active site: Lys #status predicted
F:355/Binding site: phosphate (Thr) (covalent) #status predicted
F:522/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match      92.6%; Score 50; DB 1; Length 546;
Best Local Similarity 75.0%; Pred. No. 0.078;
Matches      9;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

QY      2  TFCGTXXXYAPE 13
      |||||  ||||
Db      355  TFCGTPPEYLAPE 366

Search completed: February 18, 2006, 08:01:50
Job time : 33.4737 secs

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